The Dissertation Committee for Stephanie Lynn Johnson Certifies that this is the approved version of the following dissertation:

A GENERAL METHOD FOR MODELING COASTAL WATER POLLUTANT LOADINGS

Committee:

David Maidment, Supervisor

Mary Jo Kirisits, Co-Supervisor

Daene McKinney

Robert Gilbert

George Ward

Elizabeth Smith

A GENERAL METHOD FOR MODELING COASTAL WATER POLLUTANT LOADINGS

by

Stephanie Lynn Johnson, B.S.; M.S.

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Dedication

This work is dedicated to my family, whom I thank for their constant encouragement and support. You make my successes all the more sweet.

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I would like to acknowledge my advisors, Dr. David Maidment and Dr. Mary Jo Kirisits for their guidance and support during the course of this work. I also would like to acknowledge the other committee members for their input, in particular Dr. George Ward for his insight on the mechanics of tidal systems. Lastly, I thank my colleagues and the staff at The Center for Research in Water Resources and Edward Ling of the Texas Commission on Environmental Quality. Their day to day support was invaluable.

A General Method for Modeling Coastal Water Pollutant Loadings

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Stephanie Lynn Johnson, Ph.D.

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Supervisors: David Maidment and Mary Jo Kirisits

The focus of this work was to develop a general methodology for modeling water quality in coastal waterbodies. The methods were developed in the context of modeling bacterial total maximum daily loads (TMDLs), but the general approach is applicable to a wide variety of pollutants. The study area for this dissertation was the Copano Bay watershed, which is located on the Texas Gulf Coast. The developed approach combines simple modeling techniques, of the type recommended by state and national advisory groups, in a GIS (geographic information system) framework, resulting in a methodical, easily transferred approach. This work addresses coastal systems where water quality is a function of operations in non-tidal rivers, tidal rivers, and bays, combined with the effects of watershed contributions. An uncertainty analysis was done to quantify a subset of the variance in the modeled results. Outcomes from this work include modeling tools, a documented workflow for modeling water quality in coastal watersheds, procedures to quantify the uncertainty associated with the developed approach, insight to the factors

affecting water quality in the study area, and mean annual bacterial TMDLs for the impaired waterbodies of the Copano Bay watershed.

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Chapter 1: Introduction

1.1 Background and Motivation

Coastal watersheds are the setting where freshwater rivers meet the saline ocean. In this environment, three types of waterbodies exist. Freshwater non-tidal rivers flow into tidal rivers with increased salinity and some tidal impacts; tidal rivers then feed into bays, with longer residence times, higher salinity impacts, and greater tidal fluctuations. Modeling the water quality of these systems is complex because it requires consideration of each individual waterbody, the interactions between them, and their interaction with the surrounding watershed. The purpose of this dissertation is to model bacterial contamination within coastal systems, focusing on Copano Bay.

Over 42,000 water segments are currently classified as impaired on the Environmental Protection Agency's (USEPA) List of Impaired Waters (USEPA, 2008b). For each of these waterbodies a Total Maximum Daily Load (TMDL) study must be performed. Of the listed waters, 14% include bacteria as one of their impairments, making bacterial contamination the most frequently occurring impairment. In 2006, Texas had 399 impaired water segments on the list, and 312 of these segments were listed for violating bacteria standards (TCEQ, 2007a). So, similar to the national trend, though by a larger margin, bacterial contamination is the most frequently occurring impairment of Texas surface waters. Many of Texas's violating waters are on the Gulf Coast, due to stricter bacterial water quality standards for waterbodies classified as oyster waters.

Numerous studies have been done at the state and federal levels to address the question of bacterial TMDL development (Task Force, 2007; Chapra, 2003; NRC, 2001; Shabman et al., 2007). These reports question the necessity of performing detailed water quality modeling for TMDLs, particularly in the early phases of a project. There are indications that simple modeling methods might be just as good, if not preferable, to detailed models due to the sizable errors inherent in modeling natural systems (Petersen et al., 2008). Also, studies done with complex models have been met with much scrutiny and resistance by citizen stakeholder groups (Sullivan and Hambleton, 2007), a constituency that is critical to the TMDL process. A 2006 Task Force, commissioned by the Texas Commission on Environmental Quality (TCEQ) and the Texas State Soil and Water Conservation Board (TSSWCB), recommended the use of a three-tier system for performing bacterial TMDLs in the State of Texas (Task Force, 2007). The Task Force suggested that the majority of these studies be performed as Tier 1 or 2. The types of modeling suggested under Tiers 1 and 2 focus on simpler modeling approaches, including (as stated in Tier 2 Part 3) "… simple load duration curve, GIS [geographic information systems], and/or mass balance models."

1.2 OBJECTIVES

The focus of this work was to develop a general methodology for modeling bacteria in coastal waterbodies. The methodology was based on simple modeling techniques, yet is sufficiently rigorous to account for the complexities of a coastal system. These complexities include the interactions of continuous, generally low-flow non-tidal rivers; saline, slow-flushing tidal rivers; largely quiescent bays; and the

watershed that surrounds them. The work was set in the context of modeling bacterial TMDLs but the general methods are applicable to a variety of pollutants. The methods were developed through application to the Copano Bay system and then generalized for application to other watersheds/waterbodies along the Texas Gulf Coast and perhaps the nation's coast. To keep the modeling methods current with typical engineering practices and to make their use attractive to water quality professionals, the application of these methods was automated as much as possible. Automation used programmatic coding with tools such as web services, calculating/graphing software, and map interfaces within GIS. Though the goal of this research was to develop a simple modeling approach, efforts were made throughout the study to explore the processes that affect the prevalence of bacteria in these complex tidal systems, including spatial and temporal load variations. Particular attention was paid to the uncertainty that these processes bring to our modeling approach. A quantification of some of the uncertainties is presented.

1.3 RESEARCH QUESTIONS

The study area for this work was the Texas Gulf Coast, with particular focus on the Copano Bay system. Texas coastal systems include three types of waterbodies: non-tidal rivers that flow continuously; tidal rivers that have salinity impacts, reversing flows, and longer residence times; and bays that have large volumes compared to all but the highest flow events. The combination of these waterbodies, and their interaction with the watershed around them, creates a very complex system for water quality modeling. The first research question addressed in this dissertation was then

1. ***How can we combine simple modeling techniques to effectively model bacteria in the Copano Bay system?***

Water quality issues are a widespread concern both within the State of Texas and across the United States. These concerns encompass a variety of pollutants. Developing a methodology that is sufficiently general to be applied to a wide array of pollutants and geographical locations was desirable. Thus, the second research question was

2. ***How can this approach be generalized for application to a variety of pollutants and geographical locations?***

Simple models are attractive since they require fewer resources and their results are more easily communicated to a non-technical audience. Certain assumptions that are built into these modeling techniques, however, may cause uncertainty in their results. This is a particular concern when modeling very complex systems like those seen along the coast. The third research question attempted to address a portion of this uncertainty by exploring the processes that affect the studied system.

3. ***What are the processes that affect coastal systems and create uncertainty in our modeling results, and how can we quantify this uncertainty?***

1.4 DISSERTATION OUTLINE

This dissertation is organized into six chapters. Chapters two through five consist of four free-standing yet related papers as outlined in Table 1.1. These papers describe the research that was done to address the questions posed at the outset of this work.

Table 1.1: Dissertation Chapters/Papers

Chapter 2: Automated Load Duration Curve Creation for the State of Texas
Chapter 3: Spatial and Temporal Variations in Bacterial Loading in the Copano Bay Watershed
Chapter 4: A Model for Coastal Water Pollutant Loadings: TMDL Balance
Chapter 5: Computing Mean Annual Maximum Loads in the Copano Bay System

Chapter 6 concludes the dissertation with a description of how the work presented answers the research questions and summarizes the contributions that this work makes to science and technology. It also includes an acknowledgement of the limitations of the work and recommendations for further study. Appendices are provided to give additional insight to the methods used in the research.

Chapter 2: Automated Load Duration Curve Creation for the State of Texas

2.1 INTRODUCTION

Over 300 of the waterbodies on the 2006 Texas "303(d)" List include bacteria as an impairment (TCEQ 2007a). Under the Clean Water Act, the State must perform a Total Maximum Daily Load (TMDL) study for each of these waterbodies. A recent report commissioned by the Texas Commission on Environmental Quality (TCEQ) and Texas State Soil and Water Conservation Board (TSSWCB) recommended that the State begin bacterial TMDL studies with a simple modeling approach and progress to more complicated models only as deemed necessary. A simple model of particular interest is the load duration curve (Bacteria TMDL Task Force, 2007).

2.1.1 Duration Curves

The concept of duration curves is similar to that of cumulative frequency distributions (common statistical expressions of likelihood). Whereas a cumulative frequency distribution is an expression of the likelihood of obtaining a value less than or equal to a value of interest, however, a duration curve is a summary of the percent of time that a given value is equaled or exceeded, as shown in Equation 2.1.

Significant portions of this chapter have been previously published (Johnson et al., 2009).

$$p(x) = 1 - F(x) = 1 - P(X \leq x) = 1 - \sum_{x_i \leq X} P(X = x_i) \quad (2.1)$$

Where: $p(x)$ = exceedance probability of event x

$F(x)$ = cumulative frequency of event x

$P(x)$ = probability of event x

A common application of duration curves in the field of hydrology is the flow duration curve, representing the likelihood that a given flow is equaled or exceeded at a particular point on a stream. Flow duration curves are developed from historic flow data at the site providing a snapshot of the flow record at that location over a certain period of time. Figure 2.1, for example, shows a flow duration curve for the U.S. Geological Survey (USGS) gauge Station 08162600 over the time period from 1986 to 2003. From this figure we can see that the flow at Station 08162600 during these 17 years is greater than or equal to 14 cfs (0.48 m^3/s) 60% of the time. Flow duration curves are often segmented into flow regimes, as shown, to address varying hydrologic conditions at the site (Cleland, 2003).

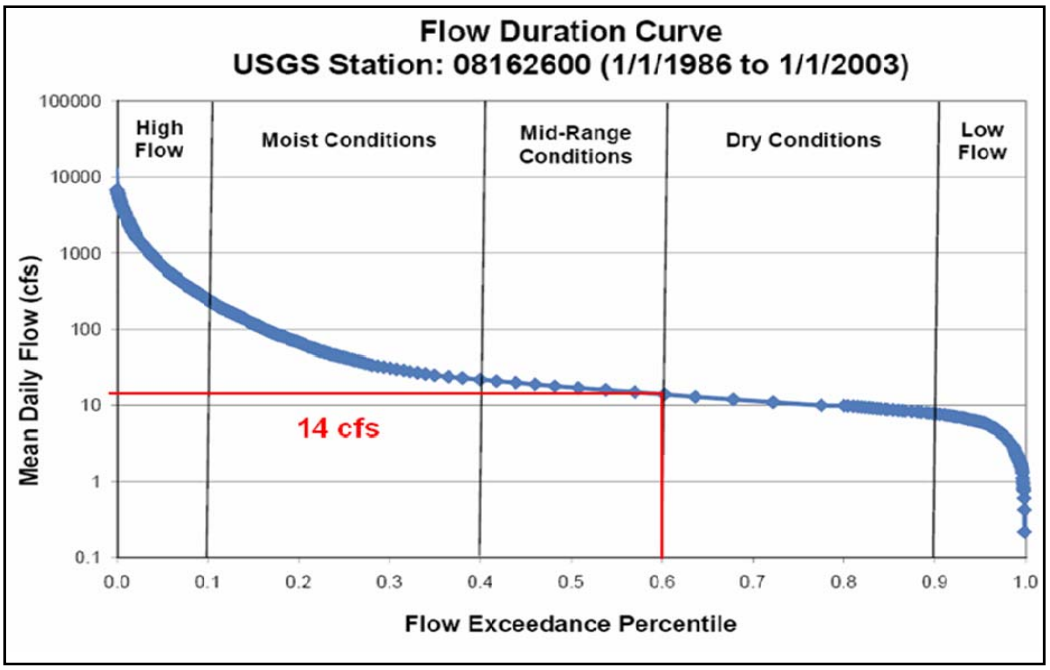


Figure 2.1: Example Flow Duration Curve

2.1.2 Load Duration Curves

Flow duration curves have a number of applications in the water resources field (Vogel and Fennessey, 1995), including water quality analysis through load duration curves. Load duration curves are developed from and operate on a similar principle to flow duration curves. Instead of addressing flows, however, load duration curves address the likelihood of equaling or exceeding a given pollutant load at a location. Curves are computed by applying the concept of mass loading (see Equation 2.2), which combines water quality and flow information to quantify the pollutant load contributed to a point on a stream by the watershed that lies above it.

$$L_i = Q_i \, x \, C_i \tag{2.2}$$

Where: L_i = mass loading of input at time i (M/T),

Q_i = input flow at time i (L^3/T)

C_i = pollutant concentration at time i (M/L^3)

Load duration curves can give insight to a number of aspects of pollutant loading such as loading patterns under various flow conditions, impacts of point versus non-point sources and the selection of best management practices (Cleland, 2002; 2003; USEPA 2007). Over the past 10 years, load duration curves have also been widely used in the calculation of TMDLs (KDHE 2008; NDEQ 2008; ODEQ 2008; Sullivan and Hambleton, 2007).

Using load duration curves to calculate TMDLs relies on the general TMDL equation

$$TMDL = \sum WLA + \sum LA + MOS \tag{2.3}$$

Where: WLA = waste load allocation (point sources)

LA = load allocation (non-point sources)

MOS = margin of safety

First, a "target" curve is developed by applying Equation 2.2. The flow duration curve (Q_i) is multiplied by the maximum desired pollutant concentration (C_i) at the site (typically the water quality criterion) and a conversion factor. The resulting curve is the

maximum pollutant load that can be experienced at the site, based on previous flow conditions, while still meeting the water quality standard (i.e., the TMDL). The target curve may be adjusted to account for a MOS as required by Equation 2.3. The MOS accounts for uncertainty between loadings and water quality. It is often expressed explicitly and then generally accounts for 5 to 10% of the TMDL. Figure 2.2 shows the fecal coliform load duration curve resulting from the flow duration curve in Figure 2.1, a water quality criterion of 400 colony forming units per 100 milliliters (CFU/100ml) (the single sample contact recreation criterion for Texas non-tidal rivers), and a 10% MOS. Results are expressed as a load, or amount, per day.

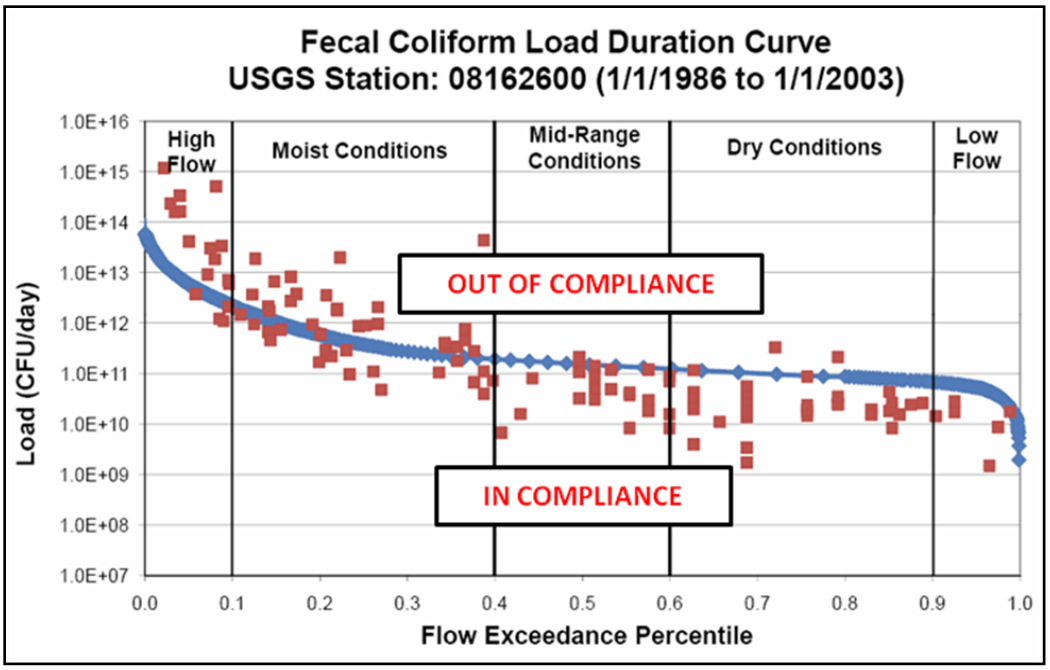


Figure 2.2: Example Load Duration Curve

After the target curve is computed, individual water quality measurements taken at the site are converted to loads (multiply the sample concentration by the observed flow on the sampling date and a conversion factor) and plotted on the same figure (see Figure 2.2). Since the target curve represents the water quality standard (potentially with a MOS), points falling above the curve are out of compliance; points falling below it are in compliance. The difference between the observed and target loads are then computed to reveal the overall load reduction needed to meet the water quality standard.

As shown in Equation 2.3, final TMDL calculations require an allocation of the target load to point (*WLA*) and non-point sources (*LA*). In a final TMDL the overall load reduction will, therefore, be subdivided to report a separate required reduction for both point and non-point sources.

2.1.3 Motivation

The flow and water quality data needed to develop load duration curves are available from various sources on the internet. Though the presence of data retrieval websites provides a convenient way to access the desired data, learning about the sites and familiarizing oneself with their use has a learning curve involved. Also, navigating through multiple web pages to retrieve the data can be a time consuming process. The use of web services can ease this process by programmatically communicating directly with the source that holds the data, removing the need to access the data retrieval web site at all.

Web Services and CUAHSI

Web services are applications that allow machines to communicate with one another over a network (World Wide Web Consortium, 2004). These services can automate the data retrieval process by accessing, retrieving, and transforming data for direct use or as input to other applications. The Consortium of Universities for the Advancement of Hydrologic Science, Inc. (CUAHSI) has developed web services for accessing the nation's water data. These services, called WaterOneFlow services, can access numerous data sources, including streamflow from the USGS. WaterOneFlow web services standardize the way that data are retrieved through functions that query a variety of sources based on defined user inputs. Examples of these functions include "GetSiteInfo", which given a site number will return information on the site and "GetValues", which given a site number, variable, and start/end date will return a time series of data for the stated variable (Maidment, 2008).

WaterOneFlow services return data in WaterML format. WaterML is a standardized eXtensible Markup Language (XML) developed as the output schema for the CUAHSI web services (Maidment, 2008). Data sources report values in a variety of formats and/or measurement units. Through the use of WaterML, WaterOneFlow services translate these data formats and return them in a standardized output, easing the development of applications that rely on the data these services return. Through the use of CUAHSI WaterOneFlow web services, the access, delivery, and use of the nation's water information is, therefore, streamlined.

Tool Creation

Since much of the development of load duration curves follows discrete, reproducible steps and the primary information needed to develop the curves is readily available online, a goal was set to create an automated procedure for computing load duration curves. A tool would be designed to retrieve flow and water quality data via web services, calculate and create curves, and determine the load reductions needed to meet the water quality standard.

The purpose of this work would be for general statewide application in the calculation of bacterial TMDLs for the State of Texas. Since point and non-point source load allocations are site specific, the output of this tool would lump point and non-point sources together. The TMDL equation for this tool would, therefore, be

$$TMDL = \sum Loads + MOS \tag{2.4}$$

Where: "*Loads*" = combined loading from both point and non-point sources

This tool would assist the TCEQ in expediting TMDL studies by providing a quick, methodical process for creating flow and load duration curves. It would also provide the basis for further TMDL study by calculating preliminary estimates of the overall (point and non-point sources combined) load reductions needed at a site.

2.2 METHODS

A load duration curve creation tool (LDCurve) was developed within the Microsoft Excel software. Automation of the tool is accomplished through Visual Basic for Applications (VBA) programming in Excel's Visual Basic Editor. Data retrieval is accomplished through the use of web services and a webscraper. Curve calculation techniques follow the U.S. Environmental Protection Agency's (USEPA) recommended procedures for using load duration curves in the development of TMDLs (USEPA, 2007).

2.2.1 Data Sources

The source of flow data for LDCurve is the USGS's National Water Information System (NWIS) (USGS, 2007d). The USGS maintains continuously monitored streamflow gauges across the country; gauge locations in the State of Texas are shown in Figure 2.3. LDCurve bases its calculations on the mean daily streamflow values measured at these USGS stations.

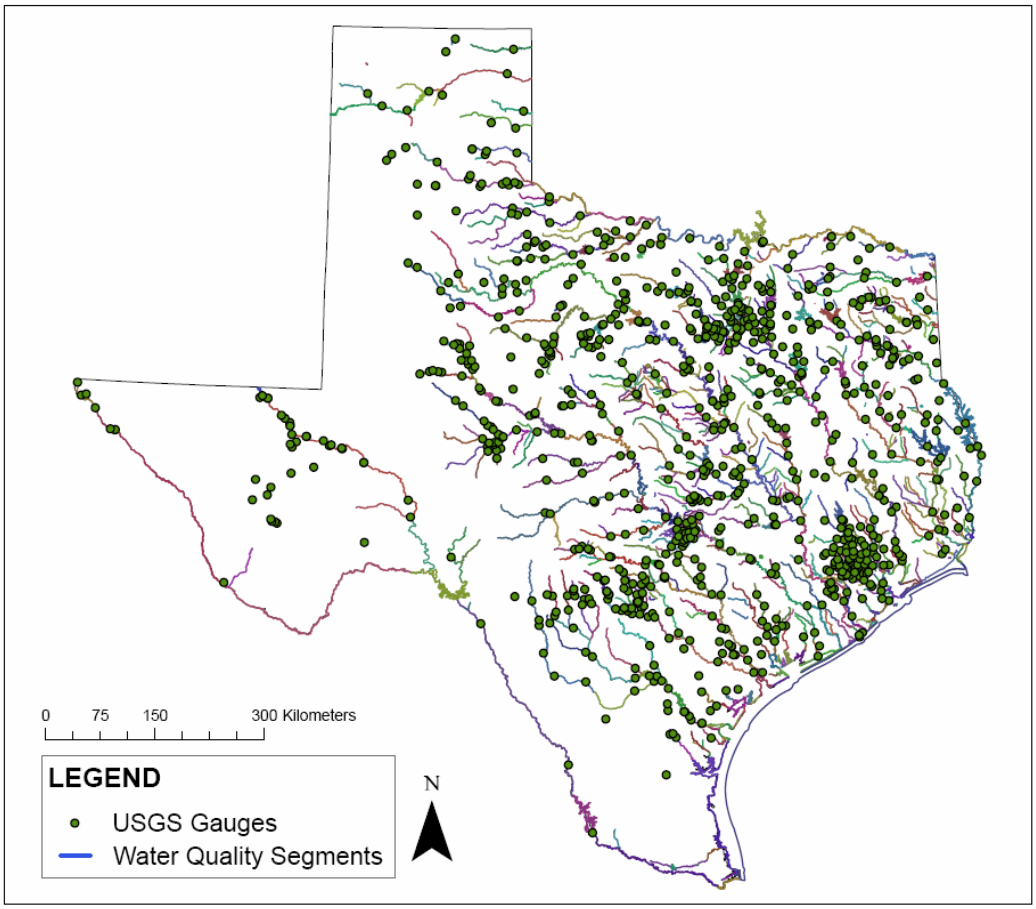


Figure 2.3: TCEQ Water Quality Segments and USGS Gauging Stations

2.2.2 Water Quality Standards

Texas waterbodies are segmented into over 800 water quality segments as shown in Figure 2.3. Water quality data are collected at surface water quality monitoring (SWQM) stations within these segments to determine the waterbody's ability to meet state water quality standards. Historic water quality data in each segment are available

online at the TCEQ Sample Data Query, SWQM website (TCEQ, 2007c), which is the source of water quality data for this project.

Water quality standards for contact recreation in non-tidal river segments (where load duration curves are used) in the State of Texas have historically addressed two bacterial indicators: *Escherichia coli* and fecal coliform. Before the year 2000, the water quality standard for rivers in the state was based on fecal coliform; after that date the indicator in non-tidal rivers changed to *E. coli*. To allow for analyses pre-, post-, and spanning the standard change, LDCurve was designed to calculate curves for both indicators.

Texas regulations also have two criteria for their bacterial water quality standards: one addressing the geometric mean and the other addressing single samples. Since the standards are most commonly violated under the single sample scenario, LDCurve was designed to use this regulation to determine compliance.

2.3 LOAD DURATION CURVE TOOL (LDCURVE)

The following section describes the general setup of the LDCurve tool. Section 2.4 illustrates the use of the tool through an example application.

2.3.1 Tool Inputs and Data Retrieval

Inputs to LDCurve include the desired TCEQ water quality segment and its associated USGS gauge station, the time period for analysis, and an explicit MOS. The user may also adjust the segmentation of the curve by changing the flow regime

percentiles (see Section 2.3.3 for details). The tool is implemented by selecting a series of code-enabled buttons in the "Station Definition" worksheet.

LDCurve accesses USGS streamflow data through the web services developed by CUAHSI and the USGS (CUAHSI, 2007). The user must, therefore, have an active internet connection (including appropriate permissions to download data) for LDCurve to work. In this case, LDCurve uses the CUAHSI NWIS Daily Value web service's "GetValues" function to retrieve streamflow data from the remote NWIS database over an internet connection.

Once initiated, the CUAHSI NWIS Daily Value web service's "GetValues" function calls the "GetValues" function of the newly developed USGS web service, GetDV (USGS, 2007c). This function accesses the NWIS mean daily streamflow time series data, translates it, and returns it in WaterML. Delivering the data in WaterML format allows LDCurve to easily parse, organize, and store the information for future use. Through the use of web services, LDCurve is therefore able to request, access, and retrieve the desired USGS streamflow data over an internet connection without ever opening a web browser.

Microsoft Excel is not able to directly access the WaterOneFlow web services. The CUAHSI HydroObjects application is, therefore, used to create a link between these two functions (Whiteaker, 2008). VBA programming in the Excel Visual Basic Editor is used to call HydroObjects, which access the web service. Information on the USGS gauge station and time period of interest is passed from LDCurve to the web service through HydroObjects. The web service then accesses, retrieves, and returns the requested data as outlined above. HydroObjects delivers the output back to LDCurve where it is manipulated for use. For the LDCurve tool to function HydroObjects must be

installed on the user's computer; a HydroObjects installation file is included with the LDCurve downloadable. The most recent version is also available via the CUAHSI website at: http://his.cuahsi.org/hydroobjects.html.

A web service is currently not available for accessing water quality data via the TCEQ SQWM Sampling Data Query website. LDCurve, therefore, accesses these data through the web query function (or "webscraper") that is built into the Excel software. The webscraper uses an internet connection to access the TCEQ website, "scrape" information from the site, and import it back to Excel as text. VBA code is then used to parse the imported data and store it for future use. For many reasons, including limited data management and increased time of execution, webscrapers are more limited applications than are web services. The LDCurve tool would, therefore, benefit from the use of web services for accessing water quality data.

Though a web service is currently not available for accessing water quality data directly from the TCEQ, CUAHSI has developed a web service to access USEPA's STORET database. STORET is the nation's repository for water quality, biological, and physical data collected by various state and federal regulatory agencies, including the TCEQ. Due to missing information in the underlying functionality of the STORET web service, some water quality data (including those of Texas) are currently not accessible but will be soon. Once the data become accessible, LDCurve may be updated to use the STORET web service to retrieve water quality data. Since LDCurve is already set up to receive data in the WaterML format, adding the use of new or different WaterOneFlow services (such as the STORET service) to its operation is easily achieved through minor re-programming. Updating the tool to use the CUAHSI STORET web service would

streamline LDCurve's operation and make it applicable to all areas of the country with water quality data in the STORET database and streamflow data in the USGS database.

2.3.2 Curve Creation

Once the streamflow data have been retrieved, VBA commands are used to calculate the cumulative frequency distribution and probability of exceedance. The flow duration curve is then created. Load duration curves are calculated by multiplying the flow duration curve by the single sample *E. coli* and fecal coliform water quality criteria of 394 and 400 CFU/100ml, respectively. These curves are then reduced by the indicated MOS to create target load duration curves.

Once the target curves are created, the user initiates adding the observed water quality data. *E. coli* and fecal coliform measurements are retrieved from the imported water quality data (from the webscraper) and combined with the mean daily streamflow on the sampling date. The result is an estimate of observed bacterial load on that day. The estimated loads are recorded in the workbook and plotted with the target curve to view compliance.

2.3.3 Calculating the Load Reduction

As a final step, the load reductions required within each flow regime and for the entire curve are calculated as the difference between the observed and target loads. Since the target curves were computed for the single sample water quality criteria, the reductions also will be based on this measure. In Texas, no more than 25% of bacterial

samples for contact recreation may have a concentration greater than the single sample criteria; seventy-five percent of samples must be less than this.

Per USEPA recommendations, the observed loads for each regime are estimated by multiplying a representative bacterial concentration by the mid-regime flow (i.e., the 25^{th} percentile flow for the 10^{th} to 40^{th} percentile regime) (USEPA, 2007). The representative concentration is chosen such that 75% of observed concentrations within that regime are equal to or less than the representative value. The representative concentration for a regime with 4 measured bacterial concentrations would, therefore, be the 3^{rd} largest concentration observed. For a regime with less than 4 samples the representative concentration would be conservatively modeled as the largest concentration observed. Target loads are defined as the load at the mid-point of each regime. Load reductions are then calculated as the difference between the observed and target loads for each regime. Similar methods are used to calculate load reductions for the entire curve, where the mid-curve flow and target load are modeled as the median value.

Determining which value most accurately reflects the required reduction at the site is left to the user's discretion. The user may choose, for example, to recommend the largest percent reduction among the modeled regimes assuming that if the most stringent value is met reductions under the other flow conditions also will be achieved. The user may also choose to disregard reductions calculated for regimes with less than 4 sampling events, noting the potential error associated with the conservative manner in which representative concentrations from these regimes were chosen.

LDCurve allows for flexibility in defining five flow regimes for the load reduction analysis. To change the regimes, the user simply inputs the desired flow

percentile ranges in the "Fecal Coliform Reductions" and "*E. coli* Reductions" tables of the workbook. LDCurve uses these user-defined ranges when performing its calculations. The vertical lines segmenting the flow and load duration curve plots must be manually adjusted by the user to properly reflect the desired segmentation.

2.4 CASE STUDY

To demonstrate LDCurve's operation and further explain the use of load duration curves in TMDL analysis, a sample application is presented. In this example, load duration curves are created for a TCEQ water quality segment that is classified as impaired for bacterial contamination on the 2006 Texas List of Impaired Waters (TCEQ, 2007a). Use of this example is for illustration purposes only and is not related to any calculation of a TMDL for regulatory purposes by the TCEQ.

Figure 2.4 shows the LDCurve setup for this example. In the "Station Definition" worksheet, the TCEQ water quality segment and correlated USGS gauge station are entered. Curves are created for the time period from January 1, 2000 to January 1, 2005 and a 5% MOS is applied (i.e., the target curve is reduced by 5% to account for an explicit MOS as shown in Equations 2.3 and 2.4). The data retrieval and curve creation steps are initiated by clicking the "Retrieve Data & Create Curves" button.

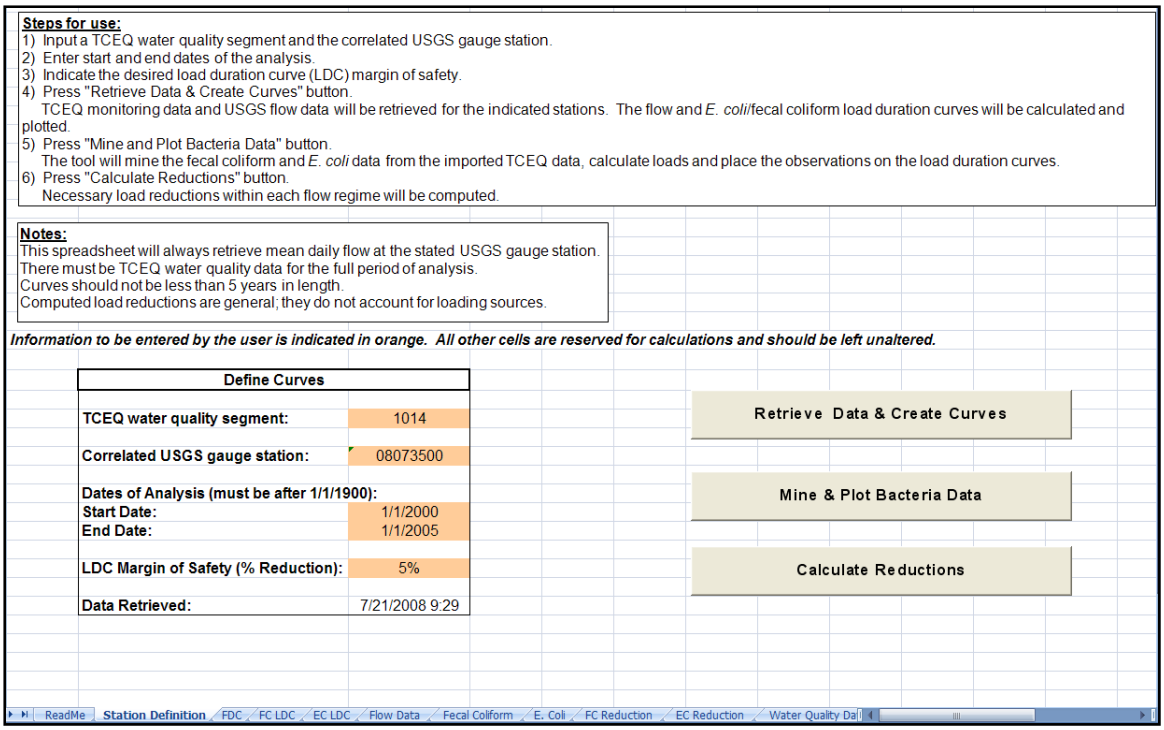


Figure 2.4: LDCurve Inputs

LDCurve uses HydroObjects to call the CUAHSI/USGS web services, which retrieve the requested mean daily streamflow data. The data are imported to the "Flow Data" worksheet, as shown in Figure 2.5. Water quality data are retrieved via the webscraper and written to the "Water Quality Data" worksheet (not pictured).

A	B	C	D	E	F	G	H	I	J	K	L
USGS Raw Data				COMPUTED							
Date	Flow (cfs)		USGS Flow (cfs)	Frequency of Flow	Probability of Flow	Cum. Distribution of Flow	Flow Exceedance Percentile	Target Single Sample Fecal Coliform Load (CFU/Day)	Target Single Sample Fecal Coliform Load w/ MOS (CFU/Day)	Target Single Sample *E. coli* Load (CFU/Day)	Target Single Sample *E. coli* Load w/ MOS (CFU/Day)
1/1/2000	31		13	3	0.00164114	0.001641138	0.998358862	1.272E+11	1.209E+11	1.253E+11	1.190E+11
1/2/2000	31		14	1	0.00054705	0.002188184	0.997811816	1.370E+11	1.302E+11	1.350E+11	1.282E+11
1/3/2000	32		16	8	0.00437637	0.006564551	0.993435449	1.566E+11	1.488E+11	1.542E+11	1.465E+11
1/4/2000	32		17	9	0.00492341	0.011487965	0.988512035	1.664E+11	1.580E+11	1.639E+11	1.557E+11
1/5/2000	29		18	2	0.00109409	0.012582057	0.987417943	1.762E+11	1.673E+11	1.735E+11	1.648E+11
1/6/2000	30		19	3	0.00164114	0.014223195	0.985776805	1.859E+11	1.766E+11	1.832E+11	1.740E+11
1/7/2000	32		20	1	0.00054705	0.014770241	0.985229759	1.957E+11	1.859E+11	1.928E+11	1.832E+11
1/8/2000	226		21	4	0.00218818	0.016958425	0.983041575	2.055E+11	1.952E+11	2.024E+11	1.923E+11

Figure 2.5: LDCurve Flow and Load Duration Curve Calculations

LDCurve calculates the cumulative frequency distribution and flow duration curve for the imported streamflow data (Figure 2.5 columns D through H). The flow duration curve is multiplied by the fecal coliform and *E. coli* water quality criteria to calculate the target load duration curves (Figure 2.5 columns I and K). The target curves are then reduced by the indicated MOS, which is 5% in this example (Figure 2.5 columns J and L).

LDCurve plots the flow and MOS-adjusted load duration curves. The flow duration curve created for this example is shown in Figure 2.6. From this curve we can see that during the years 2000 to 2005 the median flow at this USGS Station was 109 cfs (3.09 m^3/s).

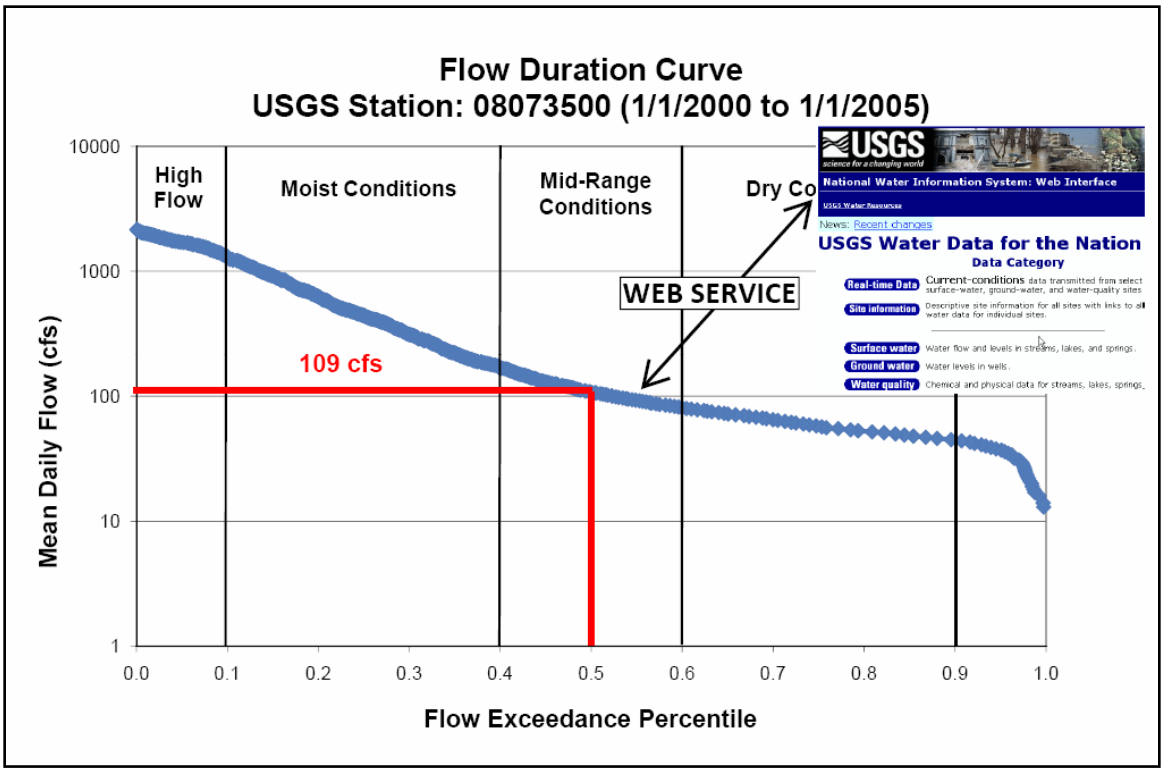


Figure 2.6: LDCurve-Created Flow Duration Curve

Observed loads are added to the load duration curve by selecting the "Mine & Plot Bacteria Data" button. LDCurve mines the bacterial measurements from the water quality data that were imported with the webscraper. Each bacterial concentration is combined with the USGS streamflow on the sampling date to compute the observed bacterial load on that date. These loads are then placed on the load duration curve as shown in Figure 2.7. In this example, the majority of observed *E. coli* loadings are out of compliance. These violations took place under all flow conditions with the most significant violations occurring during moist and mid-range conditions. Loadings of this type show no clear pattern in point versus non-point source violations.

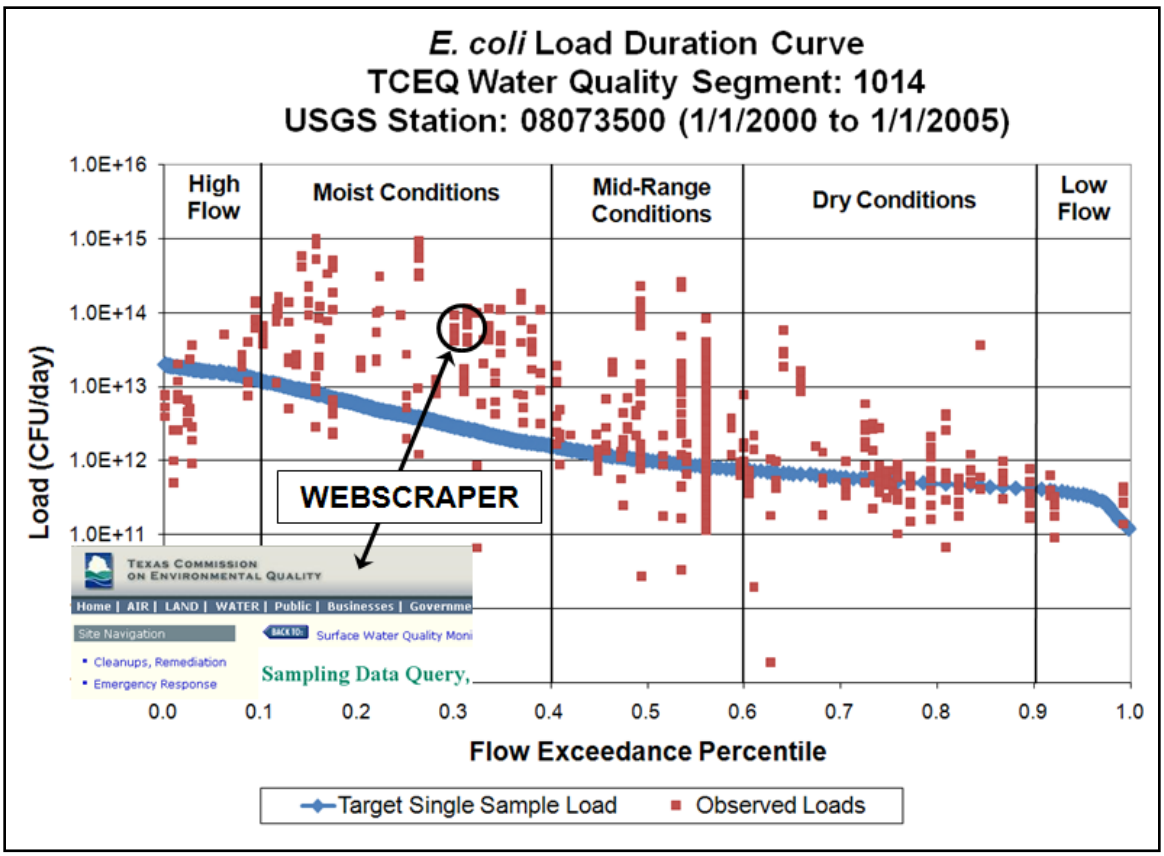


Figure 2.7: LDCurve-Created *E. coli* Load Duration Curve

Finally, the differences between the observed and target loads are used to estimate the required load reduction in each flow regime and for the entire curve. This is accomplished by selecting the "Calculate Reductions" button. Figure 2.8 shows the *E. coli* observed loads, target loads, and percent load reduction calculated for each regime in the example. Table 2.1 summarizes the information with estimates reported for all flow regimes and for the entire curve.

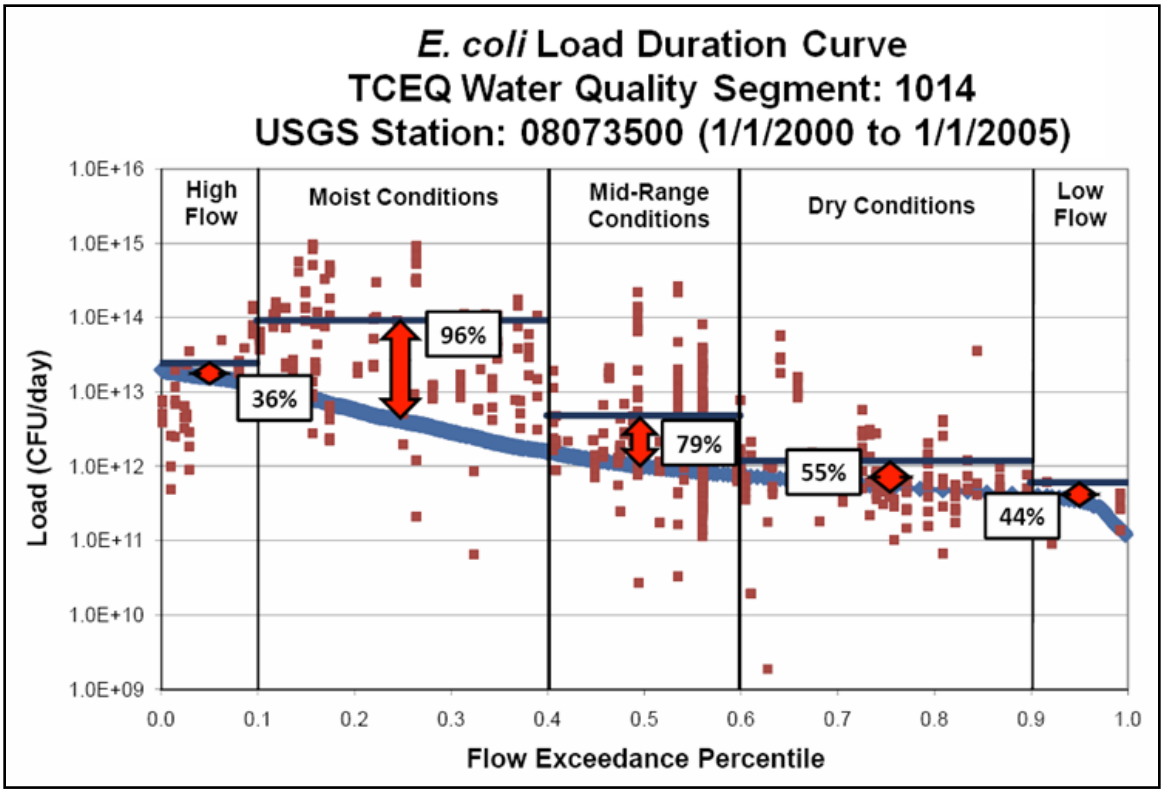


Figure 2.8: LDCurve-Estimated Observed Load, Target Load, and Overall *E. coli* Load Reductions per Regime Needed to Meet the Contact Recreation Single Sample TMDL (with 5% MOS)

Table 2.1: LDCurve-Estimated *E. coli* Loads and Overall Reductions Needed to Meet the Contact Recreation Single Sample TMDL (with 5% MOS)

***E. coli* Reductions**							
Flow Percen-tile Range	**Hydrologic Condition Class**	**No. of Samples**	**Represen-tative Concen-tration (CFU/ 100 ml)**	**Mid-Range Flow (cfs)**	**Mid-Range Observed Load (CFU/ day)**	**Mid-Range Target Load (CFU/ day)**	**% Load Reduc-tion at Mid-Range**
0-0.1	**High Flow**	40	580	1710	$2.4x10^{13}$	$1.6x10^{13}$	36%
0.1-0.4	**Moist Conditions**	145	8400	445	$9.2\ x10^{13}$	$4.1x10^{12}$	96%
0.4-0.6	**Mid-Range Conditions**	341	1800	109	$4.8x10^{12}$	$1.0x10^{12}$	79%
0.6-0.9	**Dry Conditions**	135	830	58	$1.2x10^{12}$	$5.3x10^{11}$	55%
0.9-1.0	**Low Flow**	12	670	37	$6.1x10^{11}$	$3.4x10^{11}$	44%
0-1.0	**Entire Curve**	673	2400	109	$6.4x10^{12}$	$1.0x10^{12}$	84%

For this example, LDCurve calculated a necessary overall (combined point and non-point source) *E. coli* load reduction of between 36% and 96%. The LDCurve tool created this estimate in a matter of minutes, while a detailed study would likely take months. LDCurve is not a substitute for detailed TMDL studies. Its application, however, can provide the user with a good first estimate of the overall load reduction that might be necessary in a watershed. This estimate also might be useful in guiding further work on the project.

2.5 CONCLUSIONS FOR CHAPTER 2

The tool (LDCurve) presented in this paper automates the procedure for creating flow and bacterial load duration curves and for estimating load reductions needed for water quality segments in the State of Texas. Outputs from this tool have numerous applications in the water resources field, including the preliminary analysis of bacterial TMDLs. The tool is meant as a first step in water quality analysis, providing the user with a preliminary estimate of the overall (a combination of point and non-point source) load reductions needed to meet the single sample bacterial water quality criteria. The LDCurve tool provides a methodical, reproducible procedure for performing these analyses in a matter of minutes, expediting a process that would normally take hours.

One limitation of the LDCurve tool is that it creates load duration curves for a water quality segment, not at a station. TCEQ water quality segments describe a length of stream. Water quality samples are often times taken at numerous SWQM stations within those segments. Due to limitations in downloading data from the TCEQ website, the water quality information accessed via the webscraper is imported to LDCurve by water quality segment, not by individual station. The LDCurve tool, therefore, lumps all bacteria data collected within a segment together for its calculations. USGS streamflow data are provided at a discrete location. Typically the modeled USGS gauge station does not correspond precisely to a single sampling point within the water quality segment (i.e., the segment only has one SWQM station and it is at the USGS station). Streamflows at the USGS station are, therefore, assumed to be representative of flows within the entire segment and the bacterial loads are calculated accordingly. The loads calculated with LDCurve should, therefore, be considered estimates. The results are valuable for a

general understanding of bacterial loading under various hydrologic conditions, but might not be the actual loading occurring at the site. It is up to the user's discretion to select the most appropriate USGS station for estimating flow within a given segment. With careful selection, it might be possible to reduce the error associated with the loads. Future updates to LDCurve could include methods to model individual SWQM stations instead of segments and methods to more accurately estimate the mean daily flow at the modeled location. Also, if the tool is updated to use the CUAHSI STORET web service, this issue should be resolved since the web service will retrieve data by station not segment.

The percent load reduction estimates resulting from LDCurve are intended to provide guidance on the relative amount of bacteria over-loading observed at a site. Load reductions calculated for final TMDLs must include information on allocations to point and non-point sources (see Equation 2.3). This information is site specific and, therefore, beyond the scope of the LDCurve tool. A final TMDL analysis may use results from LDCurve as the basis of more site specific work, but should not rely solely on its output for computing the bacterial TMDL.

LDCurve is currently applicable only to water quality segments within the State of Texas. Since NWIS maintains streamflow data for the entire country, however, LDCurve can easily be manipulated for application to other parts of the U.S. by developing a webscraper or web service to access online water quality data for that location. A CUAHSI web service is currently available to access the USEPA STORET database; this service is not, however, functioning to retrieve the STORET data for Texas. Once the STORET web service is functional for Texas data, LDCurve may be updated to use it for accessing water quality data. If the update is made, LDCurve should

be applicable to any area of the country where USGS flow and USEPA STORET data are available.

As developed, LDCurve is only intended for use in calculating bacterial TMDLs based on single sample water quality criteria for contact recreation in non-tidal river segments. Updating the tool for application to other pollutants or water quality standards, however, is easily attained by changing the STORET codes and/or water quality criteria included in the underlying VBA programming.

2.6 TOOL ACCESS

LDCurve, directions for its use, and all supporting materials can be downloaded free of charge from the Center for Research in Water Resources website at http://tools.crwr.utexas.edu/LDCurve.

Chapter 3: Spatial and Temporal Variations in Bacterial Loading in the Copano Bay Watershed

3.1 INTRODUCTION

Of the 399 water segments that are listed as impaired on the 2006 Texas List of Impaired Waters, more than 70% have bacteria listed as one of their impairments (TCEQ, 2007a). Bacterial contamination stems from an overloading of enteric bacteria, which come from a variety of point and nonpoint sources, such as wastewater treatment plants (WWTPs), wildlife, and runoff from agricultural activities. The ability to accurately model these loadings has historically been limited, largely due to the inherent variability in bacterial concentrations in the natural environment. The focus of this work was to gain insight to these variations in the 5,620 km^2 Copano Bay watershed of Southeast Texas.

The Copano Bay watershed contains five water quality segments, as shown in Figure 3.1. Two of the segments are in free-flowing rivers, two are in the tidally influenced downstream reaches of those rivers, and one segment comprises Copano Bay itself. Of the five segments, three are listed as impaired for bacteria on the most recent Texas 303(d) list (TCEQ, 2007a): Mission Tidal River, Aransas Tidal River, and Copano Bay. TMDL studies are being carried out for each of these segments**.**

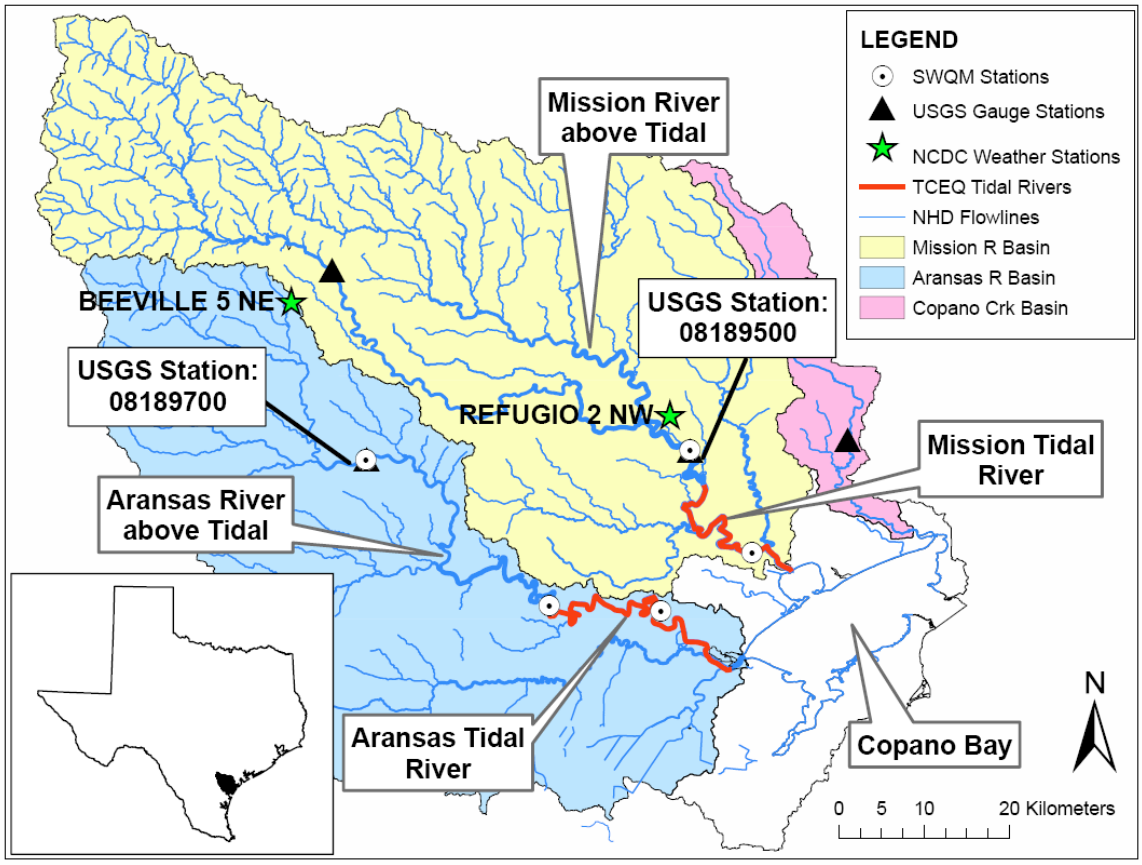


Figure 3.1: Copano Bay Watershed

Prior to this study, the water quality data available for the Copano Bay watershed included 38 years of routine sampling sponsored by the Texas Commission on Environmental Quality (TCEQ) and Texas Department of State Health Services (DSHS). This work focuses on the historic sampling of the river segments, which was sponsored by the TCEQ. In general, the river segments were monitored through quarterly samples collected at five locations in the lower half of the watershed. The purpose of this monitoring was to confirm that water quality standards were being met. While results

were considered sufficient to determine if the water segments were impaired, the spatial and temporal scales of the data were insufficient to understand and accurately model the cause and effect relationships of bacterial contamination in the study area. Requirements of a final TMDL study include the allocation of pollutant loads to point and nonpoint sources in the watershed; therefore, an understanding of this relationship is required.

Historic water quality data suggest that bacterial impairment in the Copano Bay watershed is largely a runoff-event-driven phenomenon. Low flow conditions result in minimal nonpoint source inputs and long hydraulic residence times, likely allowing for significant decay as the bacteria traverse the system. Under wet conditions, nonpoint source loads increase and residence times decrease. The average residence time in the Aransas Tidal River segment, for example, is on the order of months under low flow conditions (i.e., flows on the order of 10 cfs) and is less than a day under the highest flow conditions (i.e., flows on the order of 10^4 cfs). The combination of these factors leads to a trend of low bacterial concentrations during the majority of the year with occasional concentration spikes during runoff events. A better understanding of the bacterial concentrations under these peaking conditions was desired. Additionally, WWTPs in the watershed provide a steady effluent discharge into a system where some rivers would historically go dry periodically. Thus, a better understanding of the bacterial concentrations contributed by these WWTPs also was sought.

3.1.1 Previous Studies

Previous studies have addressed variations in bacterial loading from point and nonpoint sources. In a rural watershed in Southern Alberta, Canada, Hyland et al. (2003) found increased in-stream concentrations of fecal coliform and *Escherichia coli* in areas

with increased cattle stocking rates. The highest in-stream bacterial concentrations were found adjacent to agricultural lands after summertime rains. Other studies have pointed to runoff from urban areas (Petersen et al., 2005; Traister and Anisfeld, 2006) or to loadings from WWTPs (Tufford and Marshall, 2002) as the main causes of elevated bacterial levels. The types of land use and climate conditions in the watershed influence the loading and transport of bacteria in these systems.

When nonpoint sources are the main contributor of bacteria to a system, loadings often peak during hydrologic events such as heavy rainfall and increased runoff (Gannon and Busse, 1989; Hyland et al., 2003; Noble et al., 2003; Traister and Anisfeld, 2006). Traister and Anisfeld (2006) monitored *E. coli* concentrations in the Hoosic River Basin of Northwestern Massachusetts over several time scales including diurnal, seasonal, and intra-storm events. They showed that within a given storm, *E. coli* concentrations tracked the rise and fall of the hydrograph, though concentrations at a given water level and given site were not consistent from storm to storm. Variations in concentration within storms were similar in magnitude to variations found between seasons, while diurnal sampling showed much smaller variations in concentration (Traister and Anisfeld, 2006).

Since most WWTPs can effectively eliminate the majority of pathogens through disinfection processes, well-functioning plants typically play a much smaller role in bacterial loading than do nonpoint sources (Petersen et al., 2005). This is particularly true under wet conditions. Most WWTPs in Texas are not required to monitor bacterial concentrations directly but rather to monitor the chlorine residual in their effluent as an indication of disinfection. Since the WWTPs in the Copano Bay watershed are not required to monitor bacteria under their National Pollutant Discharge Elimination System (NPDES) permits, their effectiveness in removing bacteria is not documented.

3.1.2 Bacterial Indicators

Texas's bacterial water quality standards add an additional layer of complexity to modeling bacterial TMDLs in coastal systems. Until the late 1990s, bacterial water quality standards in the State of Texas used fecal coliform as the sole bacterial indicator. After that time, the TCEQ updated their water quality standards to reflect the 1986 USEPA recommendation to use *E. coli* as the bacterial indicator in freshwaters and enterococci as the bacterial indicator in marine waters (USEPA, 1986). If sufficient *E. coli* or enterococci data are not available for a waterbody, the historic standard for fecal coliform is applied. Texas bays that are classified as oyster-producing waters fall under the regulation of the DSHS, which continues to use fecal coliform as its bacterial indicator. From 1999 to 2003, TCEQ surface water quality monitoring sites were sampled for fecal coliform, *E. coli*, and enterococci so that a correlation between the parameters could be made and so historic data could be translated for comparison to more recent data. Since that time, sites in the Copano Bay watershed have been sampled for *E. coli* and enterococci only.

The goal of this work was to collect additional information on the underlying population of bacterial concentrations in the Copano Bay watershed, to understand temporal and spatial variations in bacterial loadings, and to improve our understanding of the relationship between the in-stream concentrations of bacterial indicators. Ideal data to address the question of spatial and temporal variation would have mapped bacterial concentrations across space at single points in time and through time at selected points in space. Temporal variability would have specifically been addressed with continuous monitoring of water quality indicators at sampling sites in the watershed. The indicators

could then have been correlated with bacterial concentrations at the time of sampling to yield a statistical estimate of the variation of bacterial concentrations over time, as a function of the variance in the water quality indicator. Such work has been demonstrated by the US Geological Survey (USGS) in Kansas rivers (Christensen et al., 2001). The sampling plan developed for this work sought to gather data as close to the ideal as possible without using continuous temporal monitoring of water quality indicators.

3.2 METHODOLOGY

3.2.1 Study Area

The Copano Bay watershed is located on the Texas Gulf Coast in Southeast Texas. The watershed is 5,620 km^2 in area. The 2001 National Land Cover Dataset (NLCD) classifies 47% of the watershed as agricultural land, 47% as forest and/or rangeland, 5% as urban, and 1% as water (USGS, 2008). Similar to most Texas segments, each of the four stream segments in the Copano Bay watershed has only one active monitoring site associated with it at any given time. TCEQ funds the collection of water quality data at these points, on average, four times per year. Figure 3.1 shows the five surface water quality monitoring (SWQM) sites that have recently been sampled in the Copano Bay watershed; Table 3.1 summarizes the period of bacterial sampling at each location. Note that Site 12947 replaced Site 12948 in 2004 because it was considered to be more representative of the Aransas Tidal River segment. Therefore, only four sites were sampled in the watershed streams at any given time.

Table 3.1: History of Bacteria Measurements in the Copano Bay Watershed

Site	Fecal Coliform			*E. coli*			Enterococci		
	N[1]	Earliest Date	Latest Date	N[1]	Earliest Date	Latest Date	N[1]	Earliest Date	Latest Date
12943	70	4/28/72	8/18/03	3	10/25/99	4/17/00	35	10/25/99	4/16/08
12944	104	11/19/70	8/18/03	37	10/25/99	4/14/08	4	10/25/99	7/11/00
12947							15	10/20/04	4/16/08
12948	72	11/19/70	8/18/03	9	10/25/99	10/8/01	15	10/25/99	7/7/04
12952	9	3/29/88	8/18/03	24	7/8/02	4/14/08			

[1] Number of bacteria samples reported in TCEQ Sampling Data Query (TCEQ 2007c).

Results of the TCEQ sampling suggest that the bacterial concentrations at these sites are log-normally distributed with a high degree of variability, which is common of bacterial concentrations in natural environments. The geometric mean and 75% probabilistic concentration (i.e., concentration that 75% of values are less than) of the data show that the Mission Tidal and Aransas Tidal River segments violate bacterial water quality standards for enterococci.

3.2.2 Sampling Approach

A team of interested parties from the TCEQ, Texas State Soil and Water Conservation Board, and the Nueces River Authority was led in developing a targeted water quality monitoring effort in the Copano Bay watershed. Based on the sampling objectives and the available budget, it was determined that 18 sampling events would be performed over a 3-year period: 11 wet events and 7 dry events. Within each of these events, 3 consecutive days of sampling would occur. Three days were chosen for consecutive sampling based on the mean annual hydraulic residence times in the non-

tidal portions of the major streams in the system, which are approximately 3 days in the Aransas River and 5 days in the Mission River (Horizon Systems, 2007). Three consecutive days of sampling would yield insight to temporal variations while not over-allocating resources.

Fourteen in-stream sampling sites were chosen as shown in Figure 3.2. Sampling locations were selected to spatially represent the upper and lower watershed, while targeting perennial streams. The lower watershed includes sites within approximately a one-day travel time of the tidal river segments under mean annual flow conditions. Four of the sites correspond with the location of existing USGS stream gauges (Sites 12944, 12952, 13660, and 20064). With the exception of Site 12948, all sampling locations are in the non-tidal rivers of the watershed. Given the location of Site 12948 at the upper extent of the Aransas Tidal River segment, its ability to consistently represent a tidal waterbody is questionable. Therefore, for the purposes of this study it is considered to be primarily a non-tidal site resulting in limited insight to bacterial concentrations in the marine-influenced portion of the watershed. Figure 3.2 also shows the location of the WWTPs in the watershed. Whenever possible, WWTP samples were collected directly from the plant's effluent pipe.

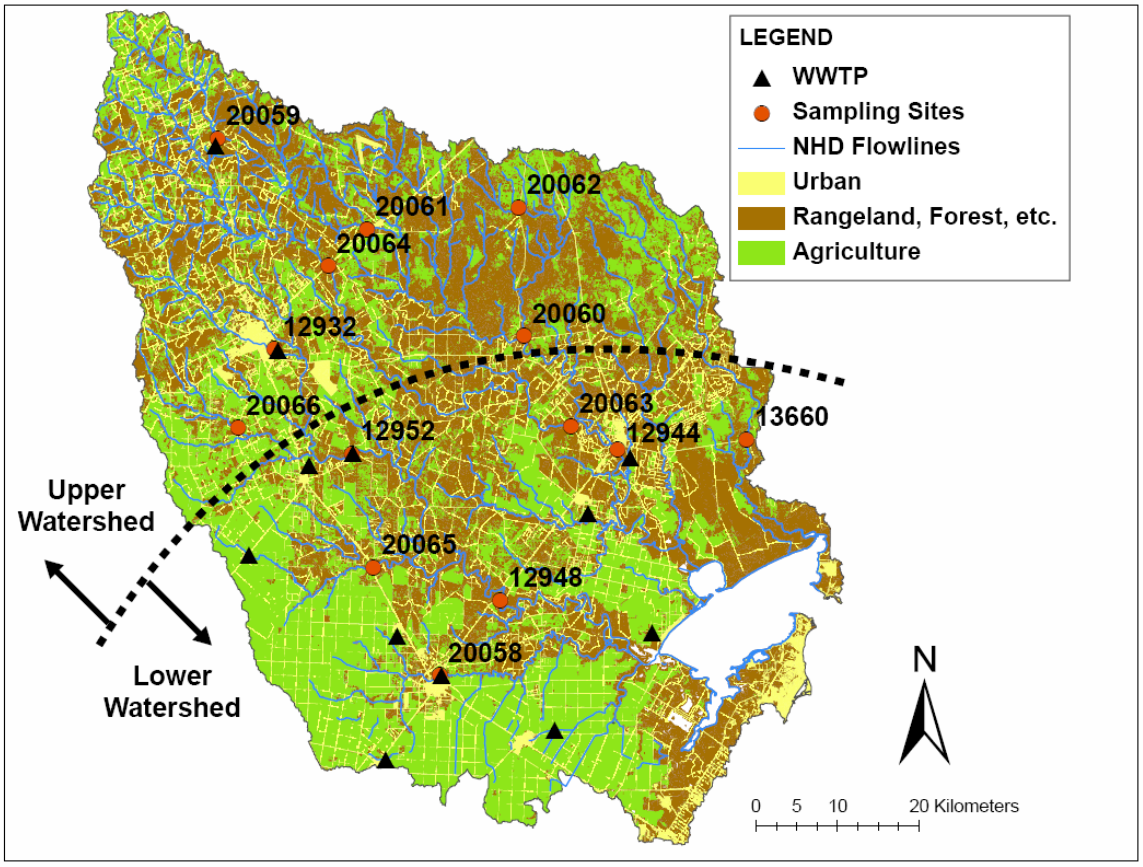


Figure 3.2: In-stream Sampling Sites, WWTPs, and General Land-Use Categories in the Watershed

3.2.3 Event Definition

For the purpose of this study, wet and dry events were defined as a function of both streamflow and precipitation. A wet event was defined as one with more than 0.5 inches of recent precipitation in the watershed, resulting in elevated flows at one or both of the two main USGS gauging stations: 08189500 Mission River at Refugio, Texas and 08189700 Aransas River near Skidmore, Texas, shown in Figure 3.1. It was reasoned

that this type of event would create runoff substantial enough to characterize the bacterial loading attributable to nonpoint sources in the watershed. Lesser runoff events likely would not have had enough flushing power to move a substantial amount of overland/nonpoint bacterial loading into the waterways. It was important to sample shortly after the rainfall event, as the goal was to capture the nonpoint source flushing from overland runoff before significant bacterial decay might occur. Dry sampling events targeted periods with little precipitation.

3.2.4 Sample Collection and Analysis

The Nueces River Authority sampled all of the in-stream sites and TCEQ staff assisted by collecting samples at the WWTP effluents when possible. River Authority staff monitored the weather and streamflow at the two aforementioned gauging stations on a daily basis. If it appeared that conditions of a wet event were approaching, the field team would mobilize to collect the necessary samples. If this determination was made with insufficient time to complete the sampling during that day, the team deployed as early as possible on the following day.

Bacterial samples were collected in pre-washed, autoclaved bottles provided by the Microbiology Laboratory at Texas A&M University – Corpus Christi, which was responsible for analyzing the samples. All field and laboratory activities followed state- and federally-approved guidelines, as outlined in the project's Quality Assurance Project Plan (Nueces River Authority, 2008). Whenever possible, samples were split for analysis of all three bacterial indicators. Fecal coliform samples were analyzed using Standard Methods 9222 D, *E. coli* using EPA 1103.1, and enterococci according to EPA 1600 (Nueces River Authority, 2008).

Some of the analyses resulted in bacterial concentrations out of the quantifiable range. This was either due to very low concentrations (reported as "<*x* CFU[colony forming units]/100 ml" with *x* depending on the volume analyzed) or due to concentrations greater than could be accurately quantified under normal laboratory procedures (e.g., ">4200 CFU/100 ml" or "estimated 4200 CFU/100 ml"). (A value of ">4200" implies that the number of colonies on the plate were too numerous to count; a value of "estimated 4200" means that the colonies were countable but out of the desired range.) In such cases, the values were rounded to the nearest integer for the statistical analyses in this paper. Values reported as "<1", for example, were analyzed as "1", whereas a value of ">4200" or "estimated 4200" was analyzed as "4200".

3.3 RESULTS AND DISCUSSION

Sampling began in the fall of 2007 and, as of January 2009, 259 in-stream samples were collected during seven events. In addition to the in-stream collections, 153 samples were collected from the watershed's WWTPs. Table 3.2 summarizes the sampling events by date, flow condition, and the number of sites/WWTPs sampled.

Table 3.2: Summary of Sampling Events

Event	Flow Conditions	Stream Sites Sampled	WWTPs Sampled
October 2-4, 2007	Dry Event	14	7
February 19-21, 2008	Dry Event	14	12
March 7-9, 2008	Wet (Mission R. & Copano Crk)/Dry (Aransas R.)	14	6
April 28-30, 2008	Wet Event	6	---
July 15-17, 2008	Dry Event	9 (5 were dry)	12
August 19-23, 2008	Wet Event	11 (3 were dry)	---
Sept 30-Oct 2, 2008	Dry Event	10	12

Mean daily flow data at the four USGS gauging stations in the watershed were obtained from the National Water Information System (USGS, 2007d). Figure 3.3 shows the average mean daily stream flow in the watershed during the sampling events (i.e., the average of flows at the four USGS gauging stations during the days of the sampling events). Note that the March 2008 event was split into two events: a wet event in the Mission River and Copano Creek basins and a dry event in the Aransas River basin. This separation was based on rainfall patterns, as discussed below. For this event, the flows in Figure 3.3 represent the average flow at the two gauging stations in each basin during the sampling days. (Note the difference in flows between the Mission and Aransas River basins.) The April 2008 event was only considered wet in the Aransas River basin. Thus, samples were only collected in this basin and the flow shown in Figure 3.3 is the average of the flow at USGS gauging stations in this area.

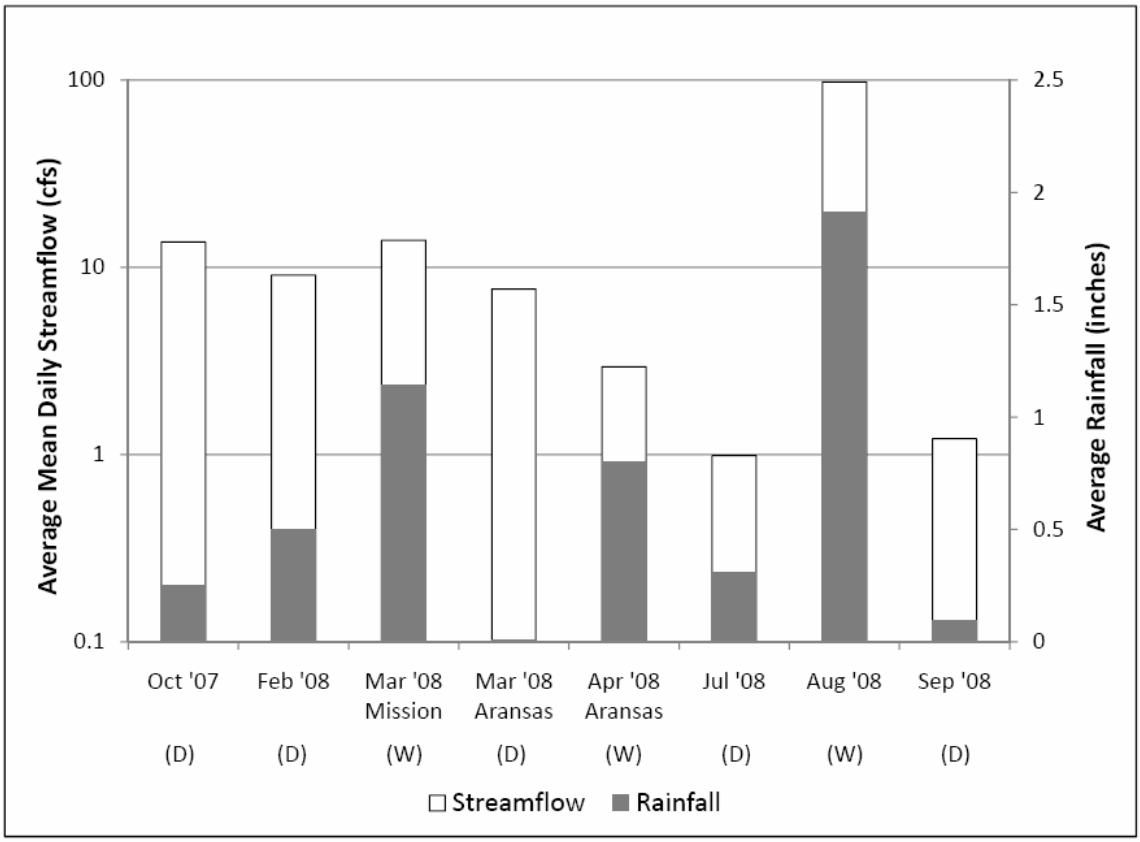


Figure 3.3: Average Mean Daily Streamflow and Rainfall during Sampling Events

Daily rainfall data were obtained at two National Climatic Data Center (NCDC) weather stations in the watershed (shown in Figure 3.1). The Beeville station was assumed to have rainfall reflective of the Aransas River basin and three sites in the upper Mission River basin (Sites 12392, 12948, 12952, 20058, 20059, 20061, 20064, 20065, 20066). The Refugio station was used to reflect conditions in the Copano Creek basin

and the majority of the Mission River basin (Sites 12944, 13660, 20060, 20062, 20063). Rainfall data at these stations are shown in Table 3.3 and summarized in Figure 3.3.

Table 3.3: Summary of Rainfall during Events

Event	Refugio Station		Beeville Station	
	Date of Most Recent Rainfall	**Amount (inches)**	**Date of Most Recent Rainfall**	**Amount (inches)**
Oct 2-4, 2007	9/30/2007	0.1	9/30/2007	0.4
Feb 19-21, 2008	2/17/2008	0.1	2/17/2008	0.9
March 7-9, 2008	3/7/2008	1.14	3/7/2008	0.01
April 28-30, 2008	4/28/2008	0.14	4/26/2008	0.8
July 15-17, 2008	7/7/2008	0.15	7/9/2008	0.47
August 19-23, 2008[1]	8/19/2008	1.29	8/19/2008	2.53
Sept 30–Oct 2, 2008	9/24/2008	0.14	9/24/2008	0.05

[1] It rained all 3 days of the August sampling event at both weather stations.

Note the difference in rainfall at the two weather stations during the March and April events. During the March sampling, only those sites represented by the Refugio weather station experienced enough rain to be considered a wet event. Sites represented by the Beeville weather station were considered to be dry. During the April wet event, the Aransas River basin was the only portion of the watershed that was sampled. This was considered to be a wet event at those sites, even though sampling occurred two days after the rainfall.

3.3.1 Spatial Variation

Figure 3.4 illustrates the spatial and temporal variation seen in the bacterial concentrations, using the March 2008 *E. coli* data as an example. For context, note that

the Texas contact recreation water quality standards for *E. coli* state that 75% of samples at each site must be less than or equal to 394 CFU/100ml; the geometric mean of the samples must be less than or equal to 126 CFU/100ml (TNRCC, 2000). Variations in fecal coliform and enterococci concentrations show a similar pattern (data not shown).

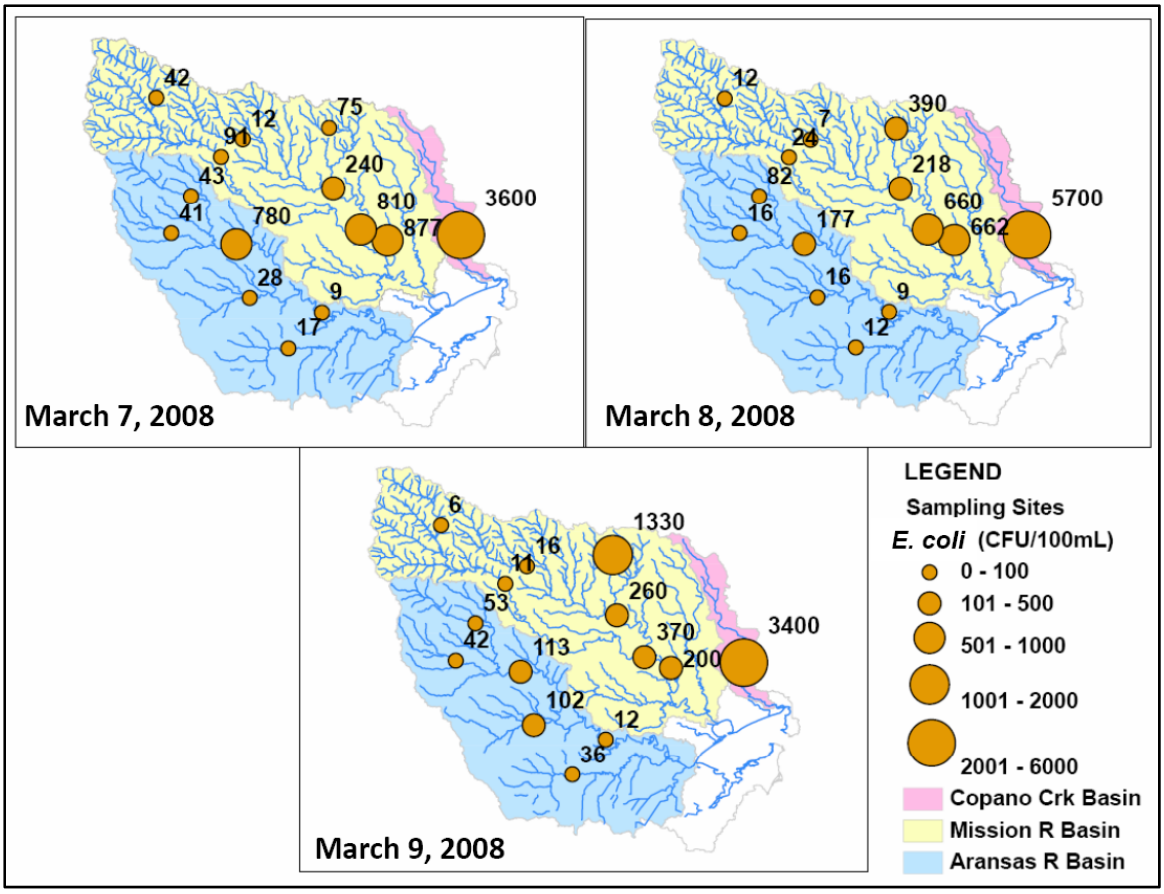


Figure 3.4: Spatial and Temporal Variations in *E. coli* Concentrations – March 2008 Sampling Event

The spatial variation in bacterial concentrations can be summarized by calculating statistics for the seven sampling events at each of the 14 in-stream sampling locations. The statistics show greater bacterial concentrations (data not shown) at sites in the lower watershed (Figure 3.2). Paired t-tests show that the geometric means of concentrations in the lower watershed are statistically different from those in the upper watershed ($p < 0.05$) for all indicators under all sampling conditions (overall, wet, and dry). This finding is similar to trends seen in other work, where bacterial loadings increase in the downstream direction (Gannon and Busse, 1989; Petersen et al., 2005). However, a definite statement cannot be made about this pattern in our work because the difference in geometric means may be a consequence of how the samples were collected rather than a trend in the spatial variation. As mentioned, the sampling crew relied upon discharge values at the mid-watershed USGS gauge stations 08189500 and 08189700 to define a wet event. By the time the hydrograph increased at these stations, the team mobilized, and samples were collected in the upper watershed, the peak runoff (and, therefore, peak bacterial concentrations) at sites above these gauges might have already occurred.

The bacterial concentrations found at Site 13660 are notable (reported as 3600, 5700, and 3400 CFU/100ml during the March 2008 event, shown in Figure 3.4). Concentrations measured at this site are consistently high and show less variation than those at the other sites. This pattern may be indicative of a nearby point source contributing a relatively constant load of bacteria to the system. However, no such source has been identified yet. Other studies have found resuspension of sediments to be a significant and regular contributor of bacteria (Jamieson et al., 2003). The ephemeral nature of Copano Creek could contribute to such a source if bacteria collect in the sediments during dry periods and intermittent flows resuspend them during wet events.

3.3.2 Temporal Variation

Wet vs. Dry Events

Figure 3.5 summarizes the temporal variations in the bacterial concentrations as a function of the hydrologic event, using the *E. coli* results as an example; similar results were seen for fecal coliform and enterococci (data not shown). The statistics reported for each event represent data collected across the entire watershed, unless they are labeled as "Aransas" or "Mission", in which case the statistics represent data from only those river basins. The box and whisker plot was constructed so that the ends of the whiskers represent the largest and smallest concentrations observed during each event. The boxes represent the 25th percentile, median, and 75th percentile concentrations. In general, wet events resulted in higher bacterial concentrations than did dry events. As noted above, the March sampling was considered a wet event for those sites represented by the Refugio weather station and a dry event for the remaining sites. Figure 3.4 depicts this event, showing increased *E. coli* concentrations on the Mission River side of the watershed.

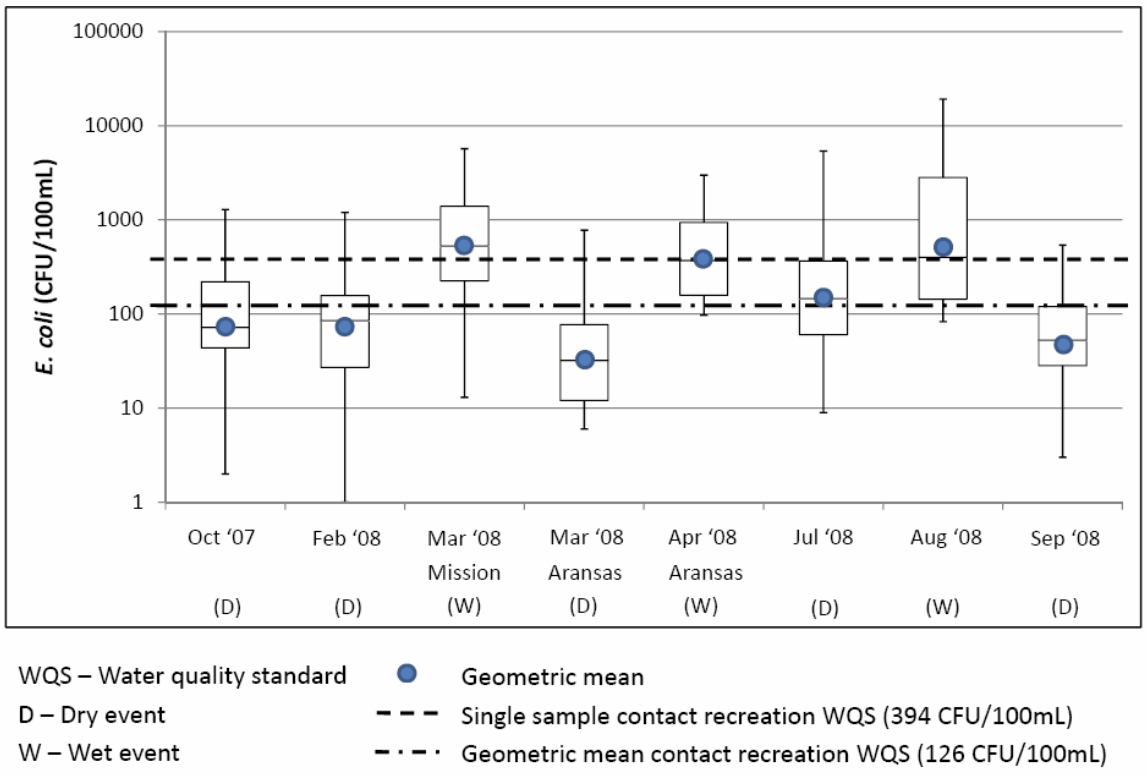


Figure 3.5: Temporal Variations in *E. coli* Statistics.

Table 3.4 shows the results of quantifying the temporal trend by combining wet and dry data and calculating the geometric means. The geometric means were then compared with a two sample t-test. p-values confirm that dry geometric mean bacterial concentrations are statistically less than wet geometric mean bacterial concentrations for all bacterial indicators. Also shown in Table 3.4 and Figure 3.5 is the fact that more *E. coli* and fecal coliform (not included in Figure 3.5) samples exceed the state freshwater contact recreation water quality standards during wet events than during dry events.

Table 3.4: Bacterial Indicators in Wet vs. Dry Events

Fecal Coliform		
	Wet Events	**Dry Events**
Geometric Mean (CFU/100ml)	535	58
Geometric Standard Deviation (CFU/100ml)	5	4
p-value	**3.0×10^{-10}**	
% > Single Sample Standard (400 CFU/100ml)	64	11
E. coli		
	Wet Events	**Dry Events**
Geometric Mean (CFU/100ml)	666	65
Geometric Standard Deviation (CFU/100ml)	5	4
p-value	**1.7×10^{-11}**	
% > Single Sample Standard (394 CFU/100ml)	77	9
Enterococci		
	Wet Events	**Dry Events**
Geometric Mean (CFU/100ml)	1524	215
Geometric Standard Deviation (CFU/100ml)	4	6
p-value	**2.6×10^{-7}**	

Relationship to Mean Daily Stream Discharge

Plotting bacterial indicator concentrations as a function of flow at individual sites shows their relationship at a point while ignoring spatial variation. This analysis was done only for those sites with USGS gauges as they were the source of flow data for this study. Table 3.5 summarizes the linear correlations between mean daily flow and bacterial concentrations at the sites. Both the flow and bacterial concentrations at these sites are log-normally distributed. When calculating linear relationships between log-normal distributions, large data values have more influence on the analysis than do smaller values and might create a deceivingly strong relationship. To reduce the potential for this deception, the analysis was performed on the natural log (ln) of the values.

Table 3.5: Correlation between ln-transformed Flow and Bacterial Concentrations

Site	ln [flow] vs. ln[Fecal Coliform]	ln [flow] vs. ln[*E. coli*]	ln [flow] vs. ln[Enterococci]
12944	0.42	0.58	0.21
12952	0.73	0.82	0.81
13660	0.06	0.33	0.10
20064	0.71	0.79	0.65
Average	0.48	0.63	0.44

Results show a uniformly positive correlation between flow and in-stream bacterial concentration. The variability and relative strength of these correlations, however, also display the inherent noise in natural systems. This is to be expected when considering bacterial concentrations, which have very large natural variances in their distribution. In general, the correlations between the *E. coli* concentrations and flow are the strongest. This is an interesting result because the sampling sites were all in non-tidal rivers where *E. coli* was chosen to replace fecal coliform as the bacterial indicator for regulatory purposes. Also of note is the low correlation between flow and bacterial concentrations at Site 13660; again, this might indicate a point source of bacteria near the site.

Figure 3.6 shows the general relationship between mean daily flow and bacterial concentrations during the August 2008 wet event at Site 12944. Similar trends were seen at Sites 12952, 13660, and 20064 (data not shown). These results are similar to those reported by Traister and Anisfeld (2006), where intra-event bacterial concentrations follow the rise and fall of the hydrograph.

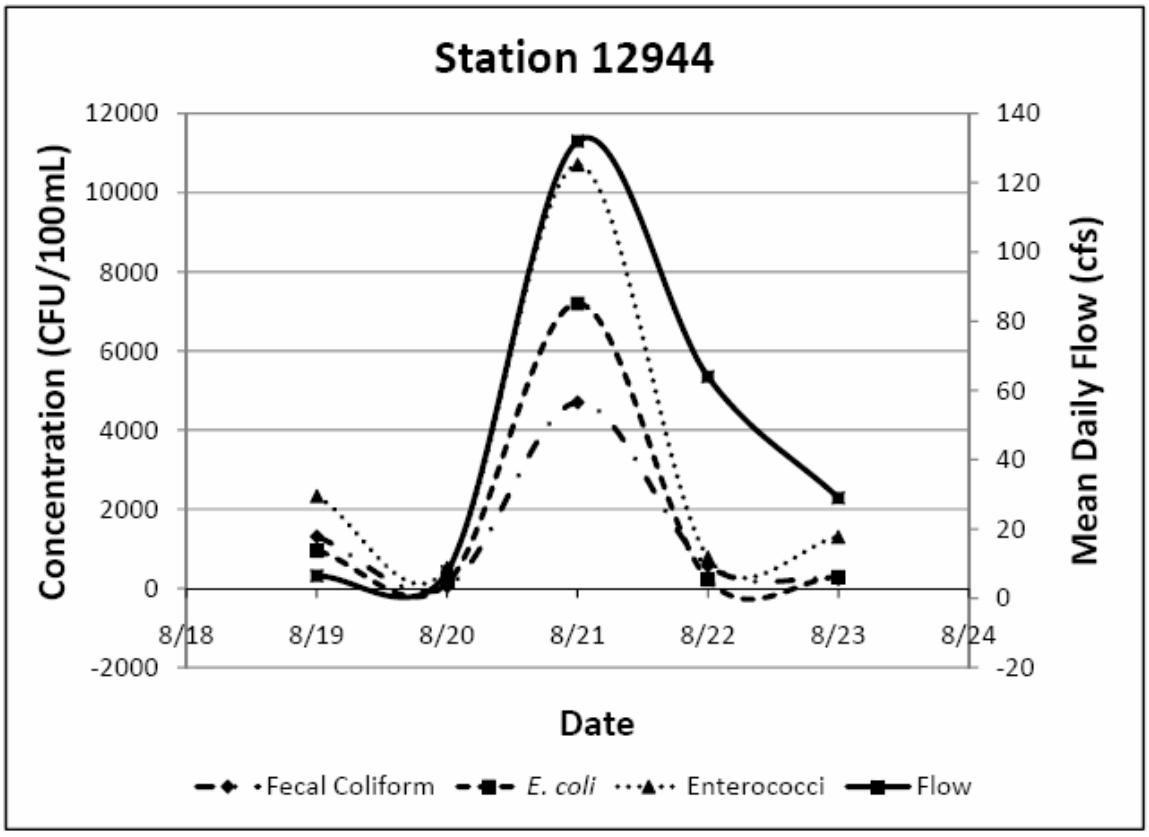


Figure 3.6: Intra-Storm Bacterial Concentrations at Site 12944

3.3.3 Correlation between Indicators

Two hundred and forty-nine of the samples were analyzed for both fecal coliform and *E. coli*; two hundred and eleven samples were analyzed for fecal coliform and enterococci. Results of these paired analyses were used to determine the relationship between the indicators in the non-tidal rivers of the watershed. Again, since the datasets to be compared both follow log-normal distributions, the concentration data was ln-transformed prior to calculations. The linear relationships between the ln-transformed data pairs are shown in Figures 3.7 and 3.8. Also shown are the overall regression

equations' coefficients of determination (R^2), F-test statistics (F), standard errors (S_e), and p-values (p).

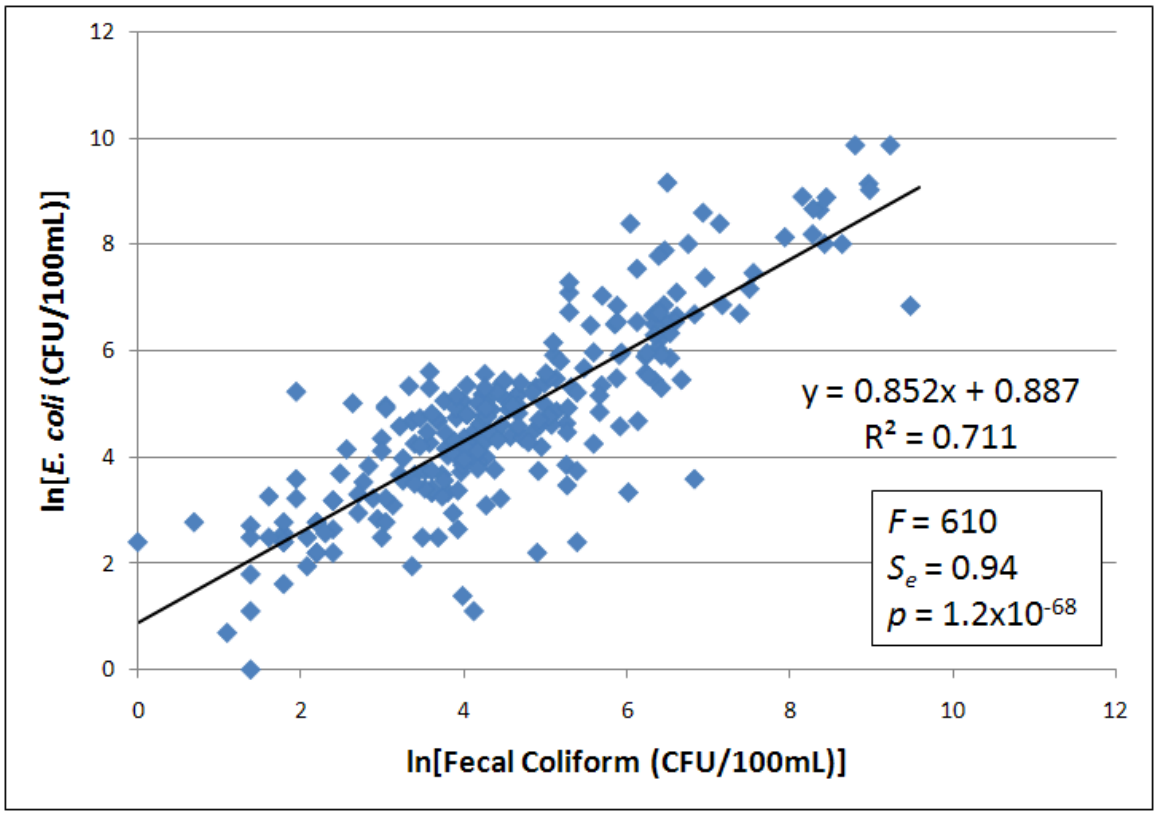


Figure 3.7: Linear Relationship between *E. coli* and Fecal Coliform Concentrations

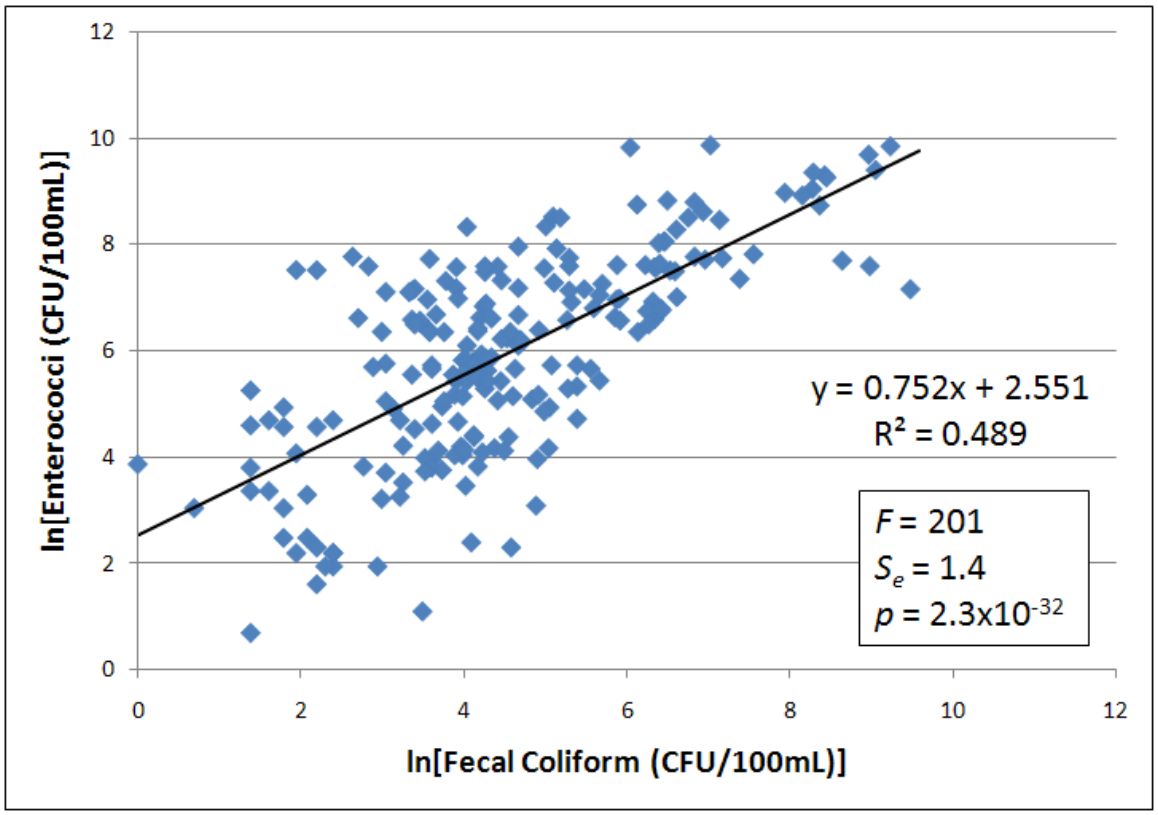


Figure 3.8: Linear Relationship between Enterococci and Fecal Coliform Concentrations

As expected, results show a positive correlation between the indicators. Also as expected, the slopes are not exactly 1.0, which would only occur if *E. coli* and enterococci concentrations changed under the same conditions and at the same rate as the fecal coliform concentrations. If this were the case, the USEPA and TCEQ would not have deemed *E. coli* and enterococci to be better bacterial indicators than fecal coliform, and the water quality standards would not have been changed. The stronger correlation between fecal coliform and *E. coli* as opposed to fecal coliform and enterococci may be

because *E. coli* is a subset of fecal coliform bacteria or because all samples were collected in freshwater.

Kloot et al. (2006) found a similar relationship between log-transformed *E. coli* and fecal coliform in a rural watershed of South Carolina with R^2 values ranging from 0.81 to 0.95. A study on beaches in Southern California showed Spearman rank correlations between log-transformed fecal coliform and enterococci concentrations ranging from 0.29-0.83; correlations were strongest under storm conditions (Noble et al., 2003).

3.3.4 Wastewater Treatment Plants

Results of sampling at the WWTPs show that some of the plants are effective in removing bacteria from their effluent, resulting in concentrations at or below 1 CFU/100ml. Other plants, however, showed consistently higher concentrations of bacteria in their effluent, some of which exceeded the receiving water's contact recreation water quality standard. In general, the mean annual flow from these plants is less than 10% of the mean annual in-stream flow, so under all but the lowest flow conditions the overall loading of bacteria from WWTPs to Copano Bay is small compared to that from nonpoint sources (discussed further in Chapter 4). However, results from this study do give insight to the bacterial loadings from these WWTPs. High concentrations from WWTP effluents in the lower watershed are of particular concern based on their proximity to the bay and the lack of time for bacterial decay in the system.

3.4 CONCLUSIONS FOR CHAPTER 3

Results from this study show spatial and temporal patterns typical of systems dominated by nonpoint sources, a strong linear relationship between ln-transformed bacterial concentrations, and surprisingly high bacterial concentrations in some of the WWTP effluents of the watershed. Results of the spatial analysis showed greater bacterial concentrations in the lower watershed than in the upper watershed; however, this result may actually be a consequence of the timing of sample collection during/after a storm event, and concentrations in the middle and upper watershed might be larger than those shown in this sampling. Continuous monitoring would give insight to these trends and should be considered for future work.

Temporal variations show a direct correlation between bacterial concentrations and flow. Geometric means of the bacterial concentrations for wet events were statistically higher than those for dry events. Analyses at the gauging stations in the watershed show a strong linear correlation between ln-transformed bacterial concentrations and mean daily flow under wet and dry scenarios. Intra-event sampling showed results similar to those of Traister and Aniston (2006), who found that bacterial concentrations follow the hydrograph at a given location. Results, however, show that concentrations are not merely a function of changing flows in the river. Flows during the October 2007 dry event were actually higher than those during the March 2008 wet event, but bacterial concentrations were greater during March. The October sampling event was 3 days after a rainfall of 0.1-0.4 inches, whereas the March event was during a rainfall of over 1.0 inch in the lower Mission River basin. Sampling during a rain event may allow for the capture of the initial flushing of bacteria in the runoff, resulting in

higher concentrations due to "first flush" conditions and less time for bacterial decay. Similarly, larger rainfall events likely suspend more bacteria in overland flow when all other conditions at the site are equal.

The linear relationship found between the ln-transformed bacteria concentrations in the Copano Bay watershed is similar to those seen in other areas of the country (Kloot et al., 2006; Lawson, 2003; Noble et al., 2003). Results of sampling at WWTPs show that bacterial loading from some of the plants might be of concern.

One limitation of this work is the general nature and limited spatial availability of flow data. More detailed flow data would allow the accurate tracking of the response of bacterial indicator concentrations to hydrologic fluctuations such as first flushes from runoff and also to see more spatial variations throughout the watershed, which would be particularly helpful in the upper watershed under this sampling method. Adding instantaneous flow measurements to the regime of this sampling plan in the coming years is recommended.

Additional limitations are mainly a consequence of limited resources and a large sampling area. As stated at the outset, ideal information for quantifying the spatial and temporal variations in bacterial concentrations would consist of many samples taken at single points in time and frequent samples taken at single points in space. Continuous monitoring at a few select points would be the best case sampling scenario. While these ambitions were not realized in the scope of this work, future sampling efforts should continue to strive toward this goal. Results of this study should be used to effectively target continuous sampling locations.

Chapter 4: A Model for Coastal Water Pollutant Loadings: TMDL Balance

4.1 INTRODUCTION

Over 42,000 water segments are currently classified as impaired on the U.S. Environmental Protection Agency's (USEPA) List of Impaired Waters (USEPA, 2008b). For each of these waterbodies, a Total Maximum Daily Load (TMDL) study must be performed. Of the listed waters, more than 14% include bacteria as one of their impairments, making bacterial contamination the most frequently occurring impairment in the nation. The 2006 Texas List of Impaired Waters classifies 399 Texas water segments as impaired, and 312 of these segments are listed for violating bacteria standards (TCEQ, 2007a). Many of the impaired segments are along the Texas Gulf Coast because coastal waters are often regulated for oyster harvesting, which results in strict bacterial water quality standards.

Coastal watersheds are the setting where freshwater rivers meet the saline ocean. In these watersheds, three types of waterbodies exist. Freshwater non-tidal river segments flow into tidal river segments with increased salinity and some tidal impacts. Tidal river segments then feed into bays, with longer residence times, higher salinity impacts, and greater tidal fluctuations. Modeling the water quality of these systems is complex because it requires consideration of each individual waterbody, the interactions between them, and their interaction with the surrounding watershed.

Numerous studies have been done at state and federal levels to address the question of bacterial TMDL development (Task Force 2007; Chapra, 2003; NRC 2001; Shabman et al., 2007). These reports question the necessity of performing detailed water quality modeling for TMDLs, particularly in the early phases of a project. There are indications that simple modeling methods might be just as good, if not preferable, to detailed models due to the sizable errors inherent in modeling natural systems (Petersen et al., 2008). Also, studies done with complex models have met resistance by citizen stakeholder groups (Sullivan and Hambleton, 2007), a constituency that is critical to the TMDL process. A 2006 Task Force, commissioned by the Texas Commission on Environmental Quality (TCEQ) and the Texas State Soil and Water Conservation Board (TSSWCB), recommended the use of a three-tier system for performing bacterial TMDLs in the State of Texas (Task Force, 2007). The Task Force suggested that the majority of these studies be performed as Tier 1 or 2. The types of modeling suggested under Tiers 1 and 2 focus on simpler modeling approaches, including (as stated in Tier 2 Part 3) "… simple load duration curve, GIS [geographic information systems], and/or mass balance models."

Using GIS to model water quality allows for the use of nationally accepted, previously created data sets, potentially saving the modeler valuable time avoiding the assembly of new data sets. The National Hydrography Dataset Plus (NHDPlus), for example, is a suite of datasets compiled in a joint effort of the USEPA and U.S. Geological Survey (USGS). The dataset includes information related to the hydrography of the United States including flowlines, catchments, monitoring locations, elevation, land use, precipitation, mean annual flow, and various other attributes (Horizon Systems, 2007). This dataset is available in a consistent format for the entire United States.

A number of models utilize GIS for calculating model inputs and parameters (the Soil and Water Assessment Tool [SWAT] (Blackland Research and Extension Center and System, 2007), HEC-GeoRAS, and HEC-GeoHMS (Army Corps, 2003; 2005), for example), using the benefits of GIS to develop inputs to free-standing modeling software. Few attempts have been made to model water within a GIS. Previous work showed the use of an ArcGIS script tool, called the schematic processor, combined with COM (component object model)-compliant dynamic linked libraries (DLLs) to model the movement of water and pollutants through a dendritic river network (Whiteaker et al., 2006). A recent study expanded that work, using the schematic processor to model bacterial contamination in a watershed of the Texas Gulf Coast (Gibson, 2006).

The objective of this work is to build on these previous GIS modeling successes to develop a general methodology for modeling bacteria in coastal waterbodies. This work is set in the context of modeling bacterial TMDLs, but the general methods are applicable to a variety of pollutants. The methodology is demonstrated through application to a case study: the Copano Bay watershed in Southeast Texas, but the general nature and GIS-focused components of the approach make it applicable to other watersheds along the Texas Gulf Coast and perhaps the nation's coast. This chapter describes the TMDL Balance model and focuses on its application to calculate watershed loading to Copano Bay. Chapter 5 continues the discussion, describing the simulation of bacterial concentrations within the tidal river sections and Copano Bay and using TMDL Balance to calculate TMDLs for the waterbodies.

4.2 METHODOLOGY

4.2.1 Study Area

The Copano Bay watershed is a 5,620 km^2 area located on the Gulf Coast in Southeast Texas. The 2001 National Land Cover Dataset (NLCD) classifies the area as 47% agricultural, 47% forest/rangeland, 5% urban, and 1% water (USGS, 2008). The watershed contains five TCEQ-defined water quality segments, as shown in Figure 4.1. The most recent Texas List of Impaired Waters lists the tidal segments of the Mission and Aransas Rivers as impaired for enterococci (TCEQ, 2007a); Copano Bay is considered impaired for fecal coliform (TCEQ, 2007a). TMDL studies are currently underway for each of these segments.

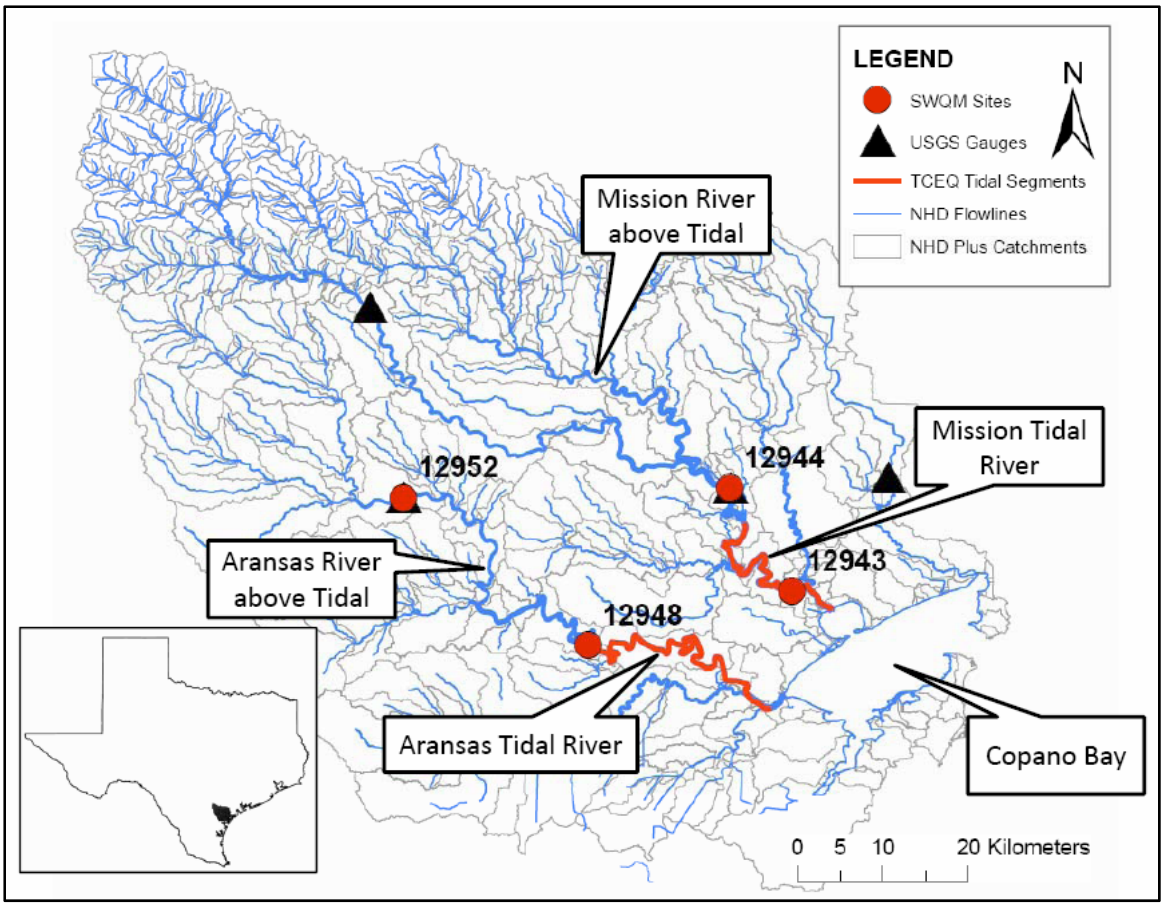


Figure 4.1: Copano Bay Watershed

The Copano Bay watershed contains four in-stream water quality monitoring sites (labeled in Figure 4.1), where the TCEQ has sponsored the collection of water quality data since 1970. A fifth monitoring site exists in the Aransas Tidal River segment, but is not shown in figure. Site 12948 has a longer period of record so the majority of water quality data describing that segment is from Site 12948. There are also four USGS stream gauge stations in the basin where continuous discharge data have been collected for 36 to 69 years. Previous work in the area showed that the sources of bacterial

contamination include feces from agricultural animals, wildlife, waterbirds, and human sources (Mott and Lehman, 2005).

4.2.2 Modeling Approach

The modeling approach used for this work is a steady state mass balance that accounts for first-order decay as bacteria travel through the system. Modeling pollutant loads in a coastal watershed is complicated by the fact that the watersheds contain both non-tidal and tidal waterbodies, which differ in their mechanics. Therefore, three separate modeling equations are used in this approach. Loading in non-tidal (freshwater) rivers is a function of point and nonpoint sources and decay, as shown in Equation 4.1.

$$L_f = \sum_{i=1}^{I} q_i c_i * e^{-k\tau_i} + \sum_{j=1}^{J} q_j c_j * e^{-k\tau_j} \quad (4.1)$$

Where: L_f = mean annual freshwater bacterial load (colony forming units [CFU]/yr)

q_i = mean annual flow of water from point source i (m^3/yr)

c_i = expected mean concentration of bacteria from point source i (CFU/m^3)

k = first-order bacterial decay coefficient (yr^{-1})

τ_i = travel time from point source i to modeled location (yr)

q_j = mean annual flow of water from nonpoint source j (m^3/yr)

c_j = expected mean concentration of bacteria from nonpoint source j (CFU/m^3)

τ_j = travel time from nonpoint source j to modeled location (yr)

Tidal river sections experience some tidal effects, which change as a function of the system's hydrology. As a consequence, the tidal rivers of the Copano Bay watershed have long residence times under all but the highest flow rates. The plug flow nature of Equation 4.1 does not fit this type of situation well, so tidal rivers are instead modeled as completely stirred tank reactors (CSTRs) as shown in Equation 4.2.

$$L^* = Q^* \frac{L_f}{Q^* + kV} \tag{4.2}$$

Where: L^* = mean annual bacterial load in the tidal river segment (CFU/yr)

Q^* = mean annual flow of tidal river segment (m^3/yr)

k = first-order bacterial decay coefficient (yr^{-1})

V = mean annual volume of tidal river segment (m^3)

The total amount of bacteria leaving the watershed and entering Copano Bay is the sum of the loads entering through the Aransas and Mission Tidal River segments and that entering from the smaller rivers (which are not regulated by TCEQ) and the land draining directly into the bay.

$$L_w = \sum L^* + L_d \tag{4.3}$$

Where: L_w = mean annual bacterial load entering Copano Bay from the watershed (CFU/yr)

L_d = $\sum L_f$ for all smaller rivers and overland flow that drain directly into Copano Bay (CFU/yr)

Copano Bay is modeled using the tidal prism approach, a steady state mass balance that calculates pollutant concentration as a function of loading to the waterbody, tidal interactions (in this case, with the adjacent Aransas Bay [Figure 5.1], which is discussed in Chapter 5), and first-order decay over one or more tidal cycles (Dyer, 1973; Fischer et al., 1979; Ketchum, 1951). Equation 4.4 shows the approach as applied in this work, where the mean annual load of bacteria exiting Copano Bay that does not return on the subsequent tide is calculated. The tidal prism approach assumes that a portion of the water that exits on the ebb tide will return on the subsequent flood tide. Formulation of the tidal prism method and the parameters that go into it are discussed in detail in Section 5.6.1.

$$L_c = C(Q_{net} + Q_a) = \frac{L_w + Q_a C_a}{(Q_{net} + Q_a) + kV}(Q_{net} + Q_a) \quad (4.4)$$

Where: L_c = mean annual bacterial load exiting Copano Bay to Aransas Bay (CFU/yr)

C = mean bacteria concentration in Copano Bay (CFU/m^3)

Q_{net} = mean annual net quantity of water exiting Copano Bay to Aransas Bay (m^3/yr)

Q_a = mean annual quantity of water entering Copano Bay from Aransas Bay on the flood tide that did not exit Copano Bay on the previous ebb tide (m^3/yr)

L_w = mean annual bacterial load to Copano Bay from the watershed (CFU/yr)

C_a = mean bacteria concentration in Aransas Bay (CFU/m^3)

k = first-order bacterial decay coefficient (yr^{-1})

V = mean annual volume of Copano Bay (m^3)

4.2.3 Schematic Processor

The schematic processor is a framework for performing hydrologic calculations in the ArcGIS environment. The schematic processor works with a schematic network, which is created from the Arc Hydro toolset (Maidment, 2002). Arc Hydro is a data model with associated tools for managing water information and supporting water analysis in GIS. The schematic network is a network of links and nodes that replicate hydrologic features on the ground. SchemaNodes represent hydrologic features, such as catchments or stream junctions. SchemaLinks dictate the connections between the nodes. The schematic processor uses the connectivity of the schematic network to pass information through a watershed, allowing the user to move water or pollutants downstream. The processor simulates this movement by assigning four values to each network feature: "received", "incremental", "total", and "passed" (Whiteaker et al., 2006).

The basic operation of the schematic processor allows the user to pass information through the watershed using simple accumulation. In other words, each feature in the network passes its "total" value to its nearest downstream neighbor. The "total" value of the downstream neighbor is the sum of all values that it "received" from the features immediately upstream of it (in this case, their "totals") plus any "incremental" value assigned to it. The schematic processor is also designed to allow the use of additional programming to apply functions to the "passed" and/or "received" values of the features

manipulating the data as it moves through the network. For this work, a function was developed to account for first-order decay as bacterial loads move through the network, by manipulating the "passed" values of the network features. The "passed" value of a feature is then equal to the "total" value minus the amount of decay. The downstream neighbor "receives" this decayed value.

The schematic processor consists of four major components, the ProcessSchematic script tool, the ProcSchematic.vbs script, the MBSchematic.dll, and any additional DLLs that may be added to account for data manipulation (Whiteaker et al., 2006). A DLL is a library of functions that can be accessed from other applications. In this way, the functionality of the MBSchematic.dll is called from within a GIS document using the ProcSchematic.vbs script. The ProcessSchematic script tool retrieves, transforms, and passes the necessary information from the GIS attribute tables to the ProcSchematic.vbs script. The script then calls the MBSchematic.dll and passes it the information needed to carry out the analysis. MBSchematic.dll performs its work (potentially calling other DLLs in the process) and passes the results through the script back to the script tool. The data are then written to the appropriate location in the GIS attribute table. Further details on this process can be found in Whiteaker et al. (2006).

4.2.4 Data Sources

National Hydrography Dataset (NHD). The primary source of data used in this work is NHDPlus, which combines the NHD (USGS, 2007a) with the National Land Cover Dataset (NLCD), the National Elevation Dataset, and the Watershed Boundary Dataset, creating an geospatial suite of integrated hydrographic data. NHDPlus contains feature classes, rasters, and attribute tables to describe the hydrologic features of a

watershed. Some of the features also have value added attributes tables, which contain additional information such as estimated mean annual velocity in stream segments, or the percent of NLCD land use in catchments. Using NHDPlus as the primary source of hydrography data not only increases the transferability of our methods but also bases our analysis on information that is accepted as the national standard.

Other Data Sources. While NHDPlus provides an excellent base for model development, many of the value added attributes (mean annual flow within each stream segment, for example) of the data are developed from general empirical relationships and intended only as estimates of actual conditions. Therefore, when possible, it is desirable to validate NHDPlus with state and local data. Additionally, NHDPlus does not contain water quality data or information on bacterial sources, so additional data sources were used for these inputs.

Water quality. The primary source of water quality data for this study is the TCEQ Surface Water Quality Monitoring Information System (TCEQ, 2007c). Historic bacteria data were downloaded for the water quality segments shown in Figure 4.1.

Streamflow. Data on discharge in the rivers of the study area were acquired from the USGS National Water Information System (NWIS) (USGS, 2007d). The USGS maintains four active gauging stations in the watershed (Figure 4.1) where streamflow and stage are measured at 15-minute intervals. NWIS is the source of the summary flow data contained in NHDPlus; NWIS daily discharge data were used directly when more detailed analyses were required.

Animal populations. The primary source of data for animal populations in the watershed is Moench and Wagner (2009). Results of this study include estimates of the number of cattle, horses, goats, sheep, hogs, poultry, turkeys, deer, and feral hogs in the

watershed. The Texas Colonial Waterbird Census is the source of data for waterbird populations (US Fish and Wildlife Service, 2003).

Wastewater treatment plants. Information on the location of wastewater treatment plants (WWTPs) in the watershed was obtained from the TCEQ. Data on the permitted and reported average flow at each plant were obtained from the USEPA Permit Compliance System (USEPA, 2008a). Bacterial concentrations in the effluent were modeled based on results of unannounced sampling at the plants, described in Chapter 3.

On-site Sewage Facilities (OSSFs). The number of septic systems (i.e., OSSFs) in the watershed was estimated from county permitting data accessed through the TCEQ On-Site Activity Reporting System (TCEQ, 2007b). Several of these systems are in communities that directly border Copano Bay. Given the impact these systems could have on the bay if they malfunction, the Texas Department of State Health Services (DSHS) reports their number and location in the Bay Sanitary Surveys and annual updates. The 2006 Copano/Aransas Bay Sanitary Survey and 2007 update report were used to locate and quantify the number of OSSFs immediately adjacent to the bay (DSHS 2006; 2007).

4.3 TMDL BALANCE

The result of this work is the TMDL Balance model, which is a steady state, mass balance model for use with the ArcGIS software. The model consists of a Visual Basic.Net DLL that contains procedures for applying the loading equations shown in Equations 4.1 – 4.4. Equation 4.1 is used to calculate the bacterial load in non-tidal rivers. Equation 4.2 then simulates the load within the tidal river sections. Equation 4.3

computes the total load of bacteria to Copano Bay from the watershed as the sum of loadings from the tidal rivers, smaller (non TCEQ-regulated) rivers, and overland flow directly into the bay. Finally, Equation 4.4 computes the load of bacteria exiting Copano Bay as a function of incoming loads, tidal interactions, and bacterial decay. Therefore, TMDL Balance extends the use of ArcGIS and the schematic processor to tidal systems, by introducing methods to account for tidal exchange.

Inputs to the watershed portion of the TMDL Balance model include estimates of point and nonpoint source pollutant loadings, which are assigned to the appropriate network SchemaNodes across the watershed. Non-tidal river SchemaLink inputs include the travel time within each segment and first-order bacterial decay coefficients. Tidal river SchemaLink inputs require mean annual segment volume, flow, and a decay coefficient. SchemaNodes in the bay portion of the model require the input of mean annual bay volume, tidal interactions, and decay coefficient. The bay SchemaLinks require the input of a travel time and decay coefficient.

The user initiates the TMDL Balance model by selecting the schematic processor application in the ArcGIS Toolbox, indicating the feature classes to be modeled, and assigning the appropriate modeling equations (see Whiteaker et al. 2006 for more details on how to use a DLL with the schematic processor). Information is then read from the appropriate attribute tables and passed to the TMDL Balance DLL as described above. TMDL Balance manipulates the data in the necessary manner (summing or decaying the loads as they move downstream) and passes the results back to the MBSchematic.dll and through the scripts, which then record the output in the target attribute table. The result of the process is an attribute table with the pollutant loads computed at each SchemaLink and SchemaNode.

4.4 CASE STUDY: FECAL COLIFORM LOADING TO COPANO BAY

To further explain the TMDL Balance model and demonstrate its use, a case study is presented. In this example the TMDL Balance model is used to calculate the mean annual loading of fecal coliform to Copano Bay. After the model is developed and calibrated, a First Order Analysis of Uncertainty is used to estimate the variance associated with certain inputs and their impact on the variance of the result. Processes within Copano Bay and the resultant bacterial concentrations are discussed in Chapter 5.

4.4.1 Modeling Framework

The first step in applying the TMDL Balance model is to create a hydrologic network for the study area. Figure 4.2 shows the schematic network that was built for the Copano Bay watershed by applying Arc Hydro tools (Maidment, 2002) to the NHDPlus data. The "Node/Link Schema Generation" function of the Arc Hydro toolbox was used to automatically create the SchemaNode and SchemaLink Types 1 and 2. This function assigns a SchemaNode to the centroid of each catchment in the watershed; these are denoted as SchemaNode Type 1 (ESRI, 2007). Type 2 SchemaNodes are then assigned at each major point along the rivers. SchemaNodes are connected with SchemaLinks to indicate hydrologic connectivity. (Appendix A includes a tutorial on creating a schematic network from NHDPlus data for use with the TMDL Balance model.)

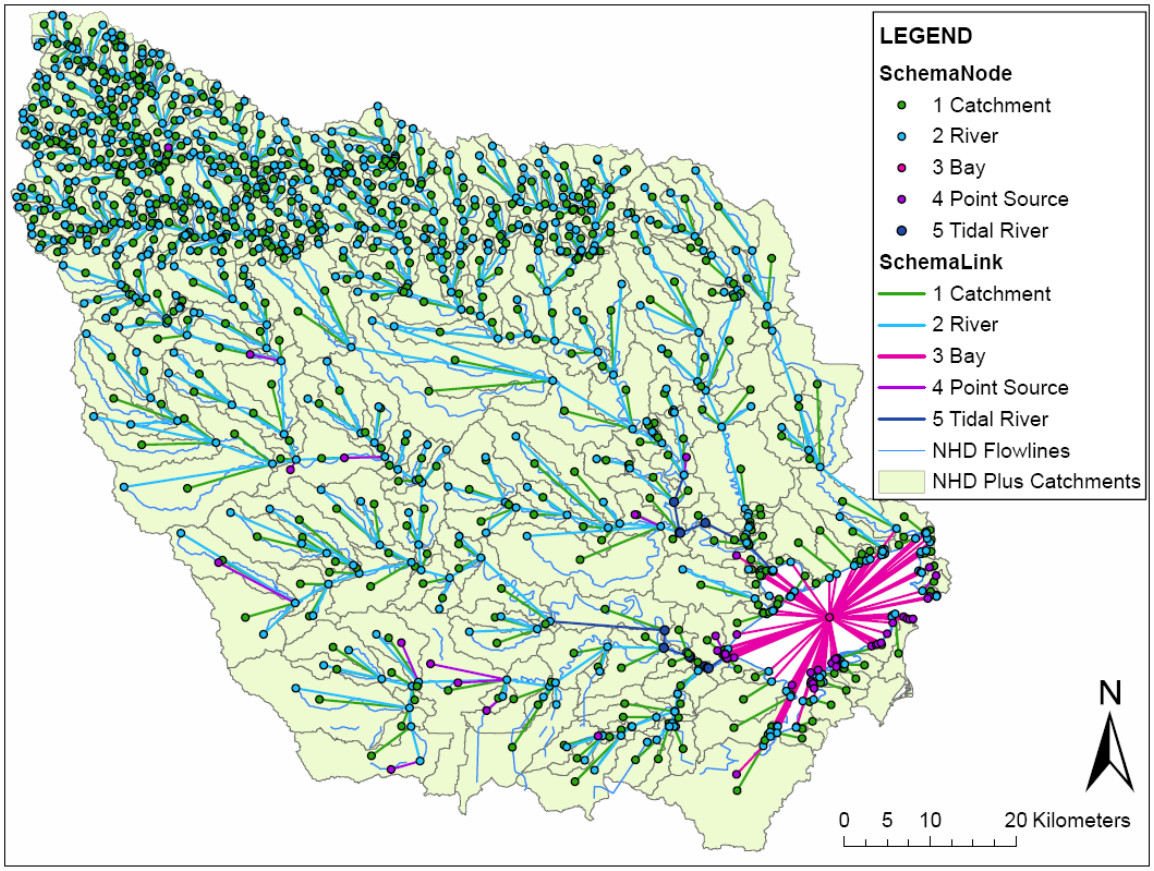


Figure 4.2: Schematic Network for Copano Bay Watershed

The schematic network is the framework upon which the schematic processor performs its calculations. The schematic processor determines which TMDL Balance equation (Equations 4.1 – 4.4) to apply to each SchemaNode and SchemaLink based on the Schema Type of the feature. For example, catchments are defined as Type 1 and non-tidal river segments are defined as Type 2, as shown in Figure 4.2. Using this approach, water and pollutants are passed through the watershed in the downstream direction as described above. Table 4.1 summarizes the SchemaNode and SchemaLink Types that are

used in this work and the equations (if any) that are applied to each. Equations are applied to the passing behavior of the features. Note that if no equation is applied to a feature, the load at that feature is simply passed downstream.

Table 4.1: SchemaNode and SchemaLink Types and Associated Modeling Equations

SchemaNode Type	**Type of Equation**	**SchemaLink Type**	**Type of Equation**
1: Catchment	---	1: Catchment	First-order decay (Equation 4.1)
2: River	---	2: River	First-order decay (Equation 4.1)
3: Bay	Tidal Prism (Equation 4.4)	3: Bay	---
4: Point Source	---	4: Point Source	---
5: Tidal River	---	5: Tidal River	CSTR (Equation 4.2)

As discussed, SchemaNode and SchemaLink Types 1 and 2 are automatically created for the watershed using Arc Hydro Tools. The watershed schematic network is connected to Copano Bay by creating and manually adding SchemaNodes/SchemaLinks Type 3 to the network. In this case, Copano Bay is modeled as a single cell so only one SchemaNode is needed. The bay SchemaNode is then connected to the watershed network through SchemaLinks. See Appendix A for details on connecting a bay to the schematic network. Point sources are included in the model by adding SchemaNodes/SchemaLinks Type 4 to the network. In the Copano Bay watershed, point sources of bacteria include fifteen wastewater treatment plants, waterbird colonies immediately surrounding the bay, and communities with failing OSSFs adjacent to the bay. These OSSFs and bird colonies are considered point sources because they add bacteria directly to the bay. Figure 4.3 shows the location of these point sources, which

are denoted with SchemaNodes Type 4 in Figure 4.2. Tidal rivers are identified by SchemaNode/SchemaLink Type 5. The spatial extents of the tidal rivers are defined by applying the TCEQ's regulatory definition to the NHDPlus flowlines.

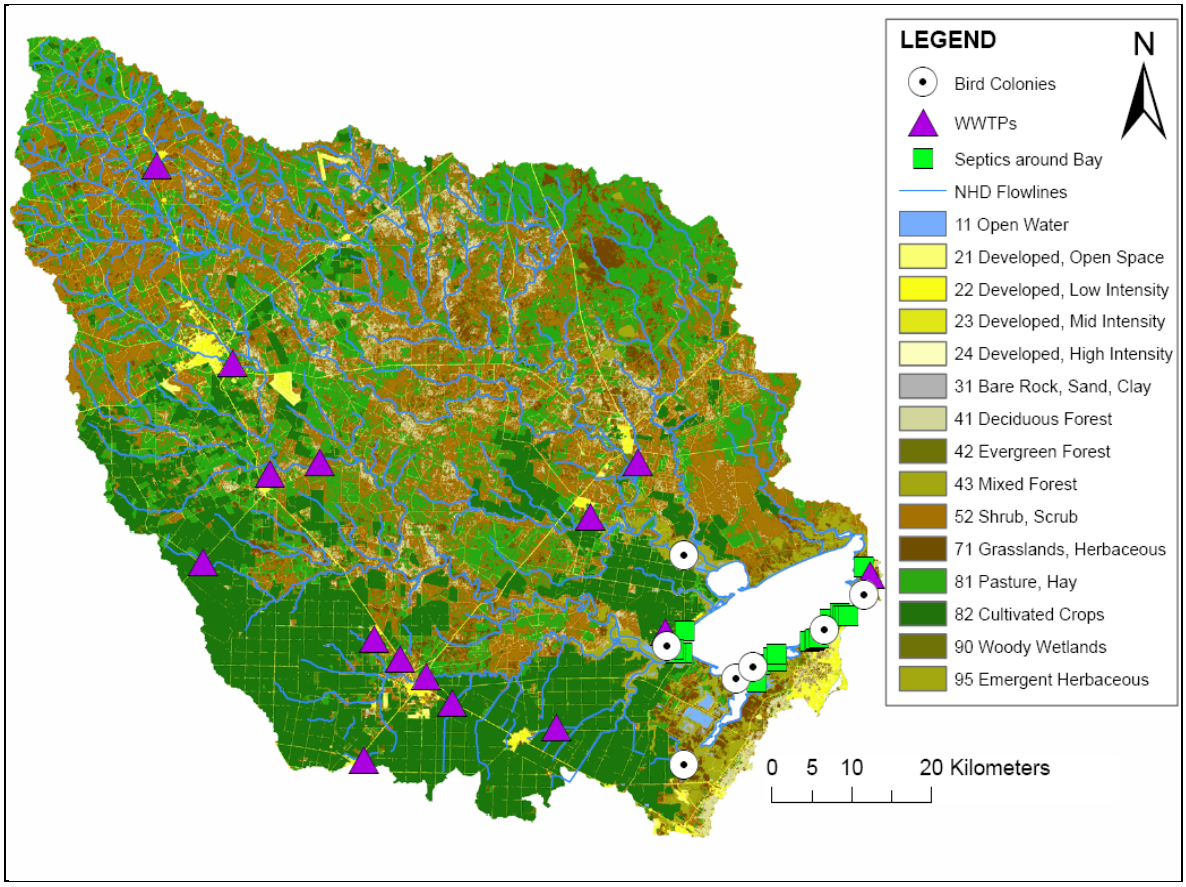


Figure 4.3: Bacterial Sources in Copano Bay Watershed

In this work, the Mission and Aransas Tidal Rivers are modeled as multiple segments as shown in Figure 4.2. Therefore, when applying Equation 4.2 to these

segments, TMDL Balance accounts for both freshwater inputs and any tidal river inputs that come from upstream. For this application, Equation 4.2 becomes

$$L_l^* = Q_l^* \frac{\sum L_f + L_{l-1}^*}{Q_l^* + kV_l} \tag{4.5}$$

Where: L_l^* = mean annual bacterial load in tidal river segment *l* (CFU/yr)

Q_l^* = mean annual flow of tidal river segment *l* (m^3/yr)

$\sum L_f$= sum of the mean annual bacterial load from freshwater sources feeding directly into tidal river segment *l* (CFU/yr)

V_l = mean annual volume of tidal river segment *l* (m^3)

See Figure 4.4 for an illustration. In the case of the most upstream tidal segment, Equation 4.5 simplifies to Equation 4.2.

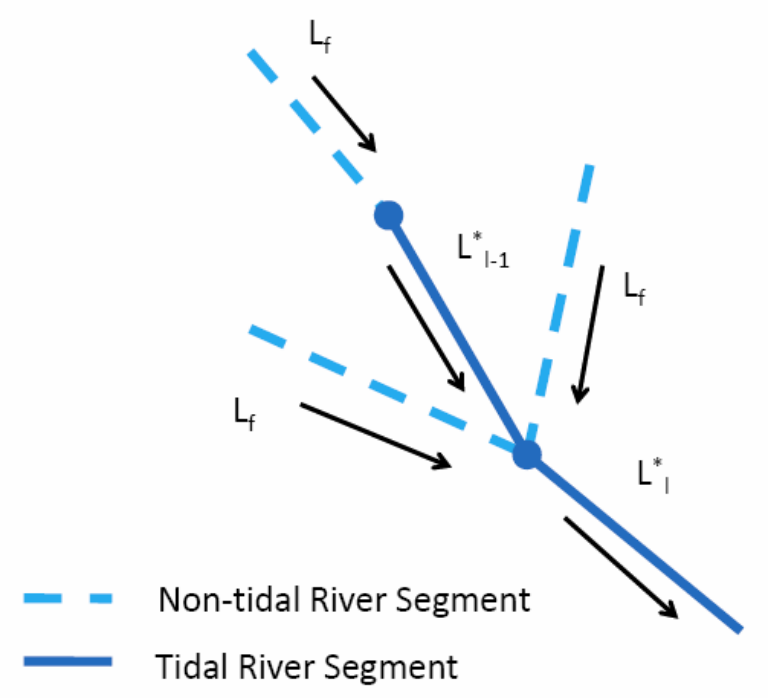


Figure 4.4: Movement of Loads through Tidal River Segments

4.4.2 Model Inputs

Once the modeling framework is created, information on the bacterial loading and hydrologic characteristics of the SchemaNodes/SchemaLinks are entered. In this case, each SchemaNode contains information on the mean annual fecal coliform load contributed at that point. For WWTPs, for example, the load is the product of the expected bacterial concentration in the plant's effluent and the mean annual flow of effluent from the plant. Nonpoint source loading from each catchment is a function of the catchment's land use/land cover (LULC), the expected mean concentration (EMC) of fecal coliform from each LULC, and the modeled mean annual runoff. This loading also

includes the estimated number of agricultural animals, wildlife, and failing OSSFs in the catchment, combined with the estimated load of fecal coliform coming from each bacterial source. A brief explanation of how these values were calculated for the Copano Bay watershed follows. Further detail is given in Appendices B and C.

Point Source Loading. The total load from point sources in the watershed is a function of the number of sources, the flow from each source, and the EMC of fecal coliform in the flow. Information on the flow rate from the WWTPs is available as either permitted maximum flow or reported mean daily flow through the USEPA Permit Compliance System (USEPA, 2008a). To more effectively represent conditions as they currently occur in the watershed, the flow from each plant was modeled as the reported mean flow rate. WWTPs in the study area are not required to routinely monitor and report bacterial concentrations in their effluent streams, leading to a lack of understanding of the plants' ability to effectively remove bacteria. In response to this problem, WWTPs were sampled as part of a targeted sampling plan developed for the watershed (discussed in Chapter 3). Results of the sampling were used to determine the EMC contributed from each WWTP, as outlined in Appendix B.

The Texas Gulf Coast has nearly thirty colonial waterbird species that regularly nest along its shores (US Fish and Wildlife Service, 2003), including those around Copano Bay. The proximity of these waterbird colonies to the bay results in bacteria from the birds being deposited directly into the bay, which leads to modeling them as point sources. Data on bird colony locations and estimates of population were obtained from the Texas Colonial Waterbird Census (US Fish and Wildlife Service, 2003). Estimates of the fecal coliform load per bird are based on an estimated 10^8 CFU/gram of

bird fecal matter and an estimated average annual weight of feces per bird as summarized by Gibson (2006).

OSSFs that are immediately adjacent to the bay also act as point sources of bacteria and have the potential to contribute significant pollutant loads to the waterbody. Because of the potential impact, the DSHS regularly monitors OSSF locations and numbers in this area (DSHS, 2006; 2007). Unfortunately, OSSF failure rates are not well quantified. Due to the mechanisms of failure and the location of these systems beneath the ground, reported system failure rates are likely to grossly underestimate the true number of malfunctions. Once a system fails, the movement of pollutants from that failure depends on a number of factors including type of failure, weather conditions, proximity to a waterbody, and the site-specific geology. The number of OSSFs failing in the area immediately surrounding Copano Bay and the amount of bacteria that moves from failed systems into the bay were estimated based on data from local officials, soil surveys, and published literature. Soil survey data classifies the area around the bay as "very limited" for use with conventional septic systems due to slow water movement in the soil, potential for flooding, and a shallow saturated zone (NRCS, 2008b). A 1978 study of nonpoint sources of bacteria in Southeast Texas estimated that, in general, 50% of OSSFs in their study area were providing little or no bacterial removal; estimates were up to 90% in some areas (Hydroscience Inc., 1978). A USEPA guidance document (2002) summarizes OSSF failure rates for 28 states. Results show that OSSF failure rates in the State of Texas range from 10-15%. Based on results of these studies and the geology of the area immediately surrounding Copano Bay, the mean annual OSSF failure rate for systems immediately surrounding Copano Bay is estimated at 50%. The estimated bacterial loading from each failing system is based on literature values

(Kaplan, 1987). The percent of loading from each failed system that reaches the bay is estimated from previous studies on the topic (Cogger et al., 1988; Hagedorn et al., 1981; Reneau and Pettry, 1975; Stewart and Reneau, 1981). Using these results, the percent of bacterial loading from a failed OSSF that will reach Copano Bay is estimated at 50%. Note that the estimated failure rate and percent of loading that will reach the bay are based on limited data and have significant uncertainty associated with them. A more thorough discussion of how loading from failing OSSFs was estimated is given in Appendix C.

Nonpoint Source Loading. Nonpoint sources of bacteria in the Copano Bay watershed include runoff from overland flow, agricultural animals, wildlife, and failing septic systems in the areas away from the immediate bay vicinity. Nonpoint source contributions are quantified per NHDPlus catchment so that data can be properly assigned to the schematic network.

Bacterial loading from overland flow is estimated as a function of each catchment's overland runoff and the EMC of fecal coliform per the land use types in that catchment. Runoff is calculated using previously developed regional regression equations (Quenzer and Maidment, 1998). These equations compute mean annual runoff as a function of mean annual rainfall for four general land use categories: urban, rangeland/forest, agriculture, and water. Land use within each catchment is categorized according to the NLCD (both 2001 and 1992 datasets were used). The flow from each catchment is then calculated as a function of these classifications and the mean annual rainfall as reported in NHDPlus. Comparing modeled values to actual flows at USGS gauge stations shows that results from the NLCD 1992 data are more accurate than those from the 2001 data. Therefore, the NLCD 1992 land classifications are used for this

study. Fecal coliform EMCs are estimated from reported literature values and previous studies in the area (Gibson, 2006; USEPA 2001; Zoun, 2003).

Bacterial loadings from agricultural animals and wildlife were computed on a per animal unit basis as discussed in Moench and Wagner (2009). The report uses local studies and animal census data to estimate the number of animals in the watershed, convert this number to animal units (an animal unit is a common unit of measurement in the agricultural sciences and is defined as 1000 pounds of animal), and compute the estimated fecal coliform loading from each animal source. For this study, the watershed-wide values were divided among the area's catchments according to the expected habitat of each animal (defined in Moench and Wagner, 2009) and NLCD 1992 data per catchment (this process is described in detail in Appendix B). For the purposes of clarity and comparison, the resultant animal populations in this paper are discussed in terms of the actual number of animals, not in animal units. Animal unit values are given in Appendix B.

The number of failing OSSFs in the area away from the bay was estimated using a similar procedure to that used for the area immediately surrounding the bay. Given the soils, depth to groundwater, and proximity to waterbodies in this area, the anticipated failure rates and bacterial loading from systems in areas away from the bay are lower. In this case, the mean annual failure rate is estimated at 15%; it is estimated that 20% of the bacterial loading from each failure will enter the nearest waterbody. Appendix C contains additional details on these estimations.

Residence Time. For this work, bacteria are assumed to travel with the water causing the bacterial residence time in each SchemaLink to be equal to the hydraulic residence time within that segment. Information on time of travel between the WWTP

and the nearest downstream junction is not available but is assumed to be minimal. Therefore, for simplicity, travel times in WWTP SchemaLinks are modeled as zero. Since bacterial loadings from sources immediately surrounding the bay (i.e., communities with OSSFs and bird colonies) are considered to be directly deposited into the bay, the travel times associated with these SchemaLinks also are modeled as zero. Note that bacterial decay within the bay is accounted for separately in the tidal prism equation, which is applied at the bay SchemaNode (Equation 4.4 and Table 4.1).

For nonpoint sources, the time of travel to Copano Bay includes the travel time through the catchment to the river via overland flow plus the travel time in the river segments. No data are available on velocity or travel times of overland flow. Therefore, the average amount of time needed for water to move via overland flow through each catchment to the nearest downstream river junction was estimated using the Soil Conservation Service (SCS) lag time method (Mays, 2001). It is assumed that bacteria move at the same rate. Calculations of overland travel times are based on the catchments' longest flow paths, average slopes, and SCS curve numbers. Appendix B describes the lag time calculations.

Times of travel through the non-tidal river segments of the watershed are modeled using NHDPlus data, regional regression equations, and estimated mean annual velocities. Flowline slope, length, upstream drainage area, and LULC in the drainage area were used as defined in NHDPlus. The estimated mean annual flow for each flowline is based on regional regression equations (Quenzer and Maidment, 1998). Mean annual velocities were calculated as described in Jobson (1996).

Tidal mechanics make travel time in tidal river sections more difficult to assess than those in non-tidal river sections. Research performed at The University of Texas

Marine Science Institute shows that under all but the most extreme flow events, tidal river segments behave more like reservoirs than free-flowing rivers (McClelland, 2008). The consequence of this is increased salinity and tidal hydraulics, along with increased residence times. For the purposes of this study, tidal river segments are simulated as CSTRs rather than as plug flow reactors. As shown in Equation 4.2, bacterial concentrations in CSTRs are calculated from the tank volume and inflow rate. Estimated tidal river volumes were computed from rough bathymetry estimates developed in collaboration with The University of Texas Marine Science Institute (McClelland, 2008). Using these data, the volumes of the Mission and Aransas Tidal River segments are estimated at 1.61×10^6 m^3 and 4.84×10^6 m^3, respectively. Combining this information with the modeled flows from the watershed, the mean annual residence times in the tidal river segments are estimated at 2 days for the Mission Tidal River and 8 days for the Aransas Tidal River. See Appendix B for more details on these calculations.

Tidal Interactions. Table 4.2 summarizes the data needed to use the TMDL Balance model to simulate bacterial concentrations in and bacterial loadings from Copano Bay. Further detail on the calculation of these values is given in Chapter 5. The mean concentrations of fecal coliform in Copano Bay and Aransas Bay (shown in Table 4.2) are computed using the "robust" regression on order statistics approach (Helsel, 2005). The large percent of non-detect data used in these analyses (73% in Copano Bay and 88% in Aransas Bay) make the values subject to interpretation.

Table 4.2: Summary of Tidal Prism Equation Inputs for Copano Bay

Parameter	Mean Value
Q_{net} (10^6 m^3/yr)	539
Q_a (10^6 m^3/yr)	1310
C (CFU/100ml)	24
C_a (CFU/100ml)	2
V (10^6 m^3)	384

4.4.3 Model Results

Total Loading in the Watershed. Table 4.3 summarizes the total mean annual fecal coliform loading computed from each of the point and nonpoint sources in the Copano Bay watershed. These values are considered non-decayed since they represent the total amount of fecal coliform contributed by each source, not the amount of fecal coliform that actually reaches Copano Bay. A unit, as presented in Table 4.3, is defined as a single animal, failing OSSF, or WWTP.

Table 4.3: Total (Non-Decayed) Fecal Coliform Load from Sources in the Copano Bay Watershed

Bacterial Source	Number of Units in Watershed	Mean Annual Loading (10^{15} CFU/yr)	% of Total (Non-Decayed) Load
Beef Cattle	66,348	207	69.5
Deer	88,850	54.5	18.3
Sheep	927	19.7	6.6
Goats	3,611	5.71	1.9
Domestic Hogs	623	5.59	1.9
Feral Hogs	37,718	2.17	0.7
Failing OSSFs (around bay)	1,090	1.19	0.4
Failing OSSFs (away from bay)	2,467	1.07	0.4
Horses	2,479	0.328	0.1
Poultry	2,620	0.341	0.1
Waterbirds	1,850	0.225	0.1
WWTPs	15	0.0646	0.02
LULC	---	0.00000008	0.0
Total (Non-Decayed) Load	---	***298***	100.0

Model Calibration in the Watershed. After the computed loads are assigned to each watershed SchemaNode and the hydrologic data are assigned to the watershed SchemaLinks, the model is run to compute the fecal coliform load to Copano Bay from the watershed while accounting for decay. For this study, the first-order decay rate was used to calibrate the model by adjusting the decay value to minimize the square error between the modeled and actual mean fecal coliform concentration at four TCEQ monitoring stations in the watershed. Actual mean concentrations were computed from historic TCEQ water quality data from December 1999 to November 2006 (the most recent TMDL assessment period) and USGS flow data.

Calibration results show a mean annual net fecal coliform decay rate in the watershed of between 1.91 $days^{-1}$ and 7.64 $days^{-1}$. The calibrated decay rate is considered net because the TMDL Balance model does not account for bacterial sources internal to the waterbodies, such as regrowth or resuspension. The calibrated decay rate consolidates all reactions internal to a waterbody into one term. The spatial distribution of the calibrated net values for the watershed is shown in Figure 4.5. The pattern of smaller decay coefficients in the lower versus upper watershed might indicate the presence of unaccounted for contributions in the lower watershed (such as regrowth or groundwater sources of bacteria). However, it could also imply that waters in the upper watershed are more hostile to bacterial cells. Given the natural variability in bacterial decay rates and the limited data available for model calibration and/or the direct measurement of decay, conclusions about the spatial variation cannot be made from these results.

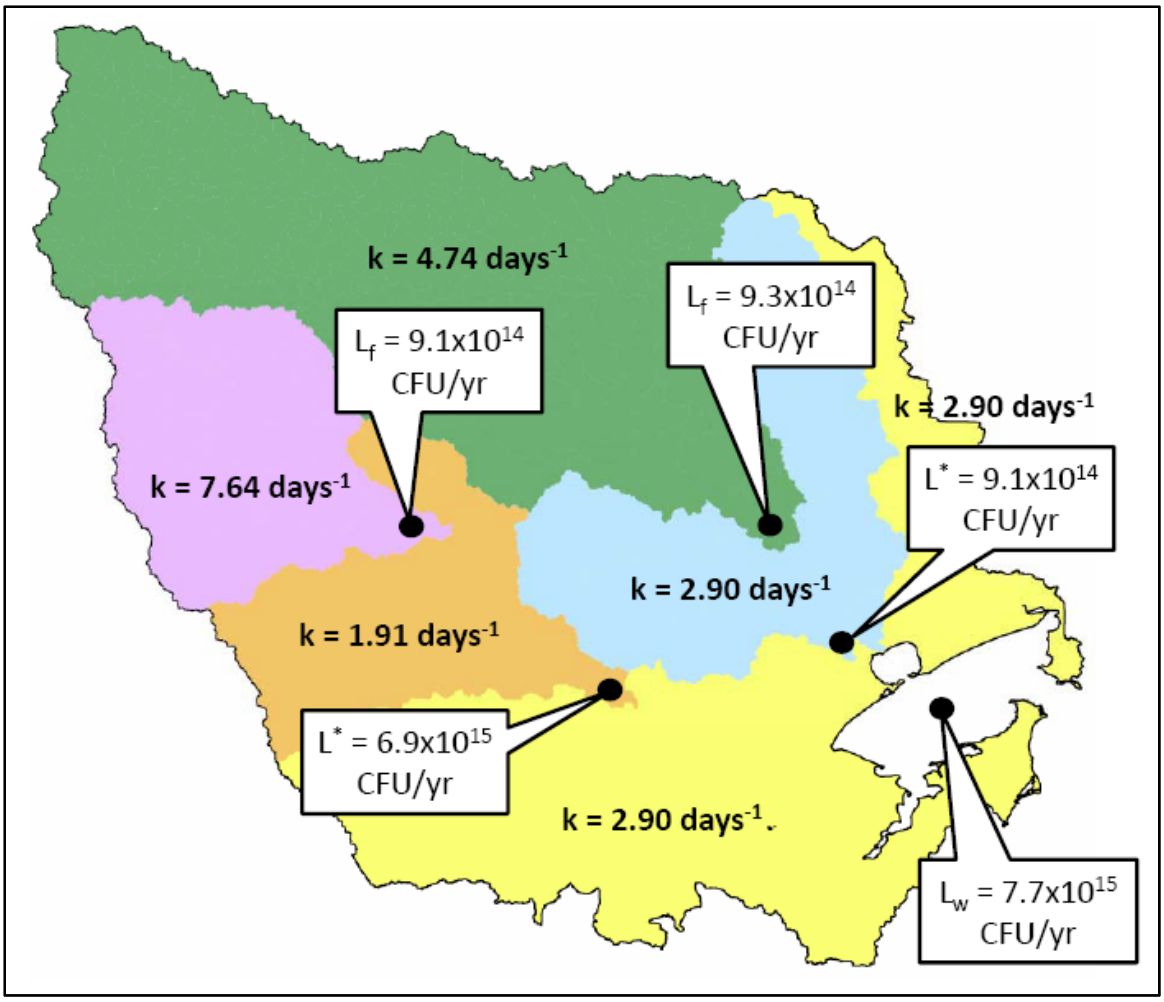


Figure 4.5: Net Annual Decay Coefficient and Mean Annual (Decayed) Fecal Coliform Loading from the Copano Bay Watershed

Fecal Coliform Load from the Watershed. The calibrated TMDL Balance model results in a mean annual loading of fecal coliform from the watershed to Copano Bay of 7.65×10^{15} CFU/yr, as shown in Figure 4.5. Mean loadings at calibration points throughout the watershed are also shown in this figure. Table 4.4 summarizes the top

five sources of fecal coliform to the bay when bacterial decay is considered. Each remaining source accounts for less than 2% of the total load.

Table 4.4: Fecal Coliform Loads (Decayed) from Major Sources in the Copano Bay Watershed

Bacterial Source	**Mean Annual Loading (10^{15} CFU/yr)**	**% of Overall (Decayed) Loading**
Beef Cattle	3.94	51.5
Deer	1.59	20.8
Failing OSSFs (around bay)	1.19	15.5
Sheep	0.35	4.5
Waterbird Colonies	0.23	2.9
Total Overall Load	***7.65***	100.0

Comparing Table 4.4 with Table 4.3 shows the impact that decay has on the bacterial loading from the watershed to Copano Bay. For example, beef cattle account for nearly 70% of the overall bacterial loading in the watershed (Table 4.3). However, their spatial distribution results in significant bacterial decay as the bacteria move through the river system and, under mean annual conditions, their contribution is reduced to 52% at the bay (Table 4.4). In contrast, the fecal coliform loadings from sources that border the bay (i.e., failing OSSFs immediately adjacent to the bay and waterbird colonies) have a much greater impact than might be expected from examining non-decayed loads. Results of this analysis show that bacterial loading from human sources is slightly less than what was found during a bacterial source tracking study done in Copano Bay in 2003-2004. Source tracking results showed that (depending on the analysis method) between 22% and 48% of *E. coli* isolates found in the bay were from human sources

(Mott and Lehman, 2005). The analysis estimates that the fecal coliform contribution is approximately 17% from human sources (failing OSSFs away from the bay account for about 1.4% of the total load).

It is important to note that the modeling scenario addressed in this paper considers fecal coliform loading under mean annual conditions. However, given the nature of the hydrology of the Copano Bay system, the mean annual condition is rarely experienced. Data at the watershed's USGS gauge stations show that the area is typically under low-flow conditions, with periodic high flow events (USGS, 2007d). Average conditions are seldom seen. As discussed in Chapter 5, Copano Bay is not violating the bacterial water quality standards under mean conditions. Trends in bacteria concentrations instead point to violations under high flow events that flush bacterial contamination from the watershed. Under these conditions, the hydraulic residence time in the watershed's rivers is on the order of one to five days. Therefore, during high flow events the bacteria will have less time to decay before they reach the bay and a much larger portion of the watershed will contribute viable bacteria to the bay. Therefore, it is anticipated that the non-decayed loadings shown in Table 4.3 are potentially more reflective of the sources of bacterial loading during violations than the decayed loads in Table 4.4.

Model Calibration in Copano Bay. Similar to the watershed loading portion of the model, the first-order decay coefficient is used to calibrate the TMDL Balance model within Copano Bay itself. The model parameters shown in Table 4.2 are combined with the results of the watershed loading calculation in Equation 4.4 and the first-order decay rate (k) is solved for directly. The resulting k value represents the net annual decay of fecal coliform within Copano Bay, reflecting all internal losses and additions. In this case, calibrating the model resulted in a k value of 0.21 $days^{-1}$. The literature shows first-

order decay coefficients for fecal coliform that are typically between 0.2 and 12 $days^{-1}$ (Brissaud et al., 2000). Thus, the value computed is near the minimum of this range. It is important to note that the calibrated value is the net decay, while those presented in the literature address pure decay (i.e., losses due to die-off, grazing, settling, etc.). The fact that the calibrated k value is at the minimum end of the expected range might indicate the presence of internal loadings of bacteria that were not explicitly accounted for in the model setup (i.e., regrowth, resuspension, groundwater inputs), indicating that the pure decay rate in the bay would be larger. This result was anticipated at the outset of the modeling exercise and is the main reason that the k value was chosen as the calibration coefficient.

4.4.4 Uncertainty in Watershed Loading Results

Modeling bacterial contamination in coastal systems is a complex problem, with much uncertainty involved. The lack of data to fully support these models and the inherent variability of bacteria in natural systems are the main reasons that simple modeling approaches, such as TMDL Balance, are recommended (Bacteria TMDL Task Force, 2007; Chapra, 2003; National Research Council, 2001; Shabman et al., 2007). Quantifying all of the potential uncertainties associated with using the TMDL Balance model to simulate the mean annual fecal coliform load to Copano Bay is beyond the scope of this work. Exploring a small portion of these uncertainties, however, will give insight to the larger variability.

Recent sampling in the Copano Bay watershed shows that in-stream fecal coliform concentrations are highly variable, both temporally and spatially (Chapter 3). A major driver of the temporal variation is the hydrology of the system in the time

surrounding the sampling event. To quantify the impact of variance in in-stream fecal coliform concentrations and streamflow on the mean annual pollutant load contributed to Copano Bay, a First Order Analysis of Uncertainty was performed. Complete details of this analysis and how the variance of the independent variables was calculated are shown in Appendix D.

The First Order Analysis of Uncertainty approach assumes that Equations 4.1 - 4.4 properly reflect the relationship between the dependent and independent variables of the TMDL Balance model so that the mean of the result is a function of the mean of the model inputs. The variance of the dependent variable is then a function of the variance of each of the independent variables, the impact that a change in the independent variables has on the dependent variable, and any correlation between the independent variables (Chow et al., 1988; Kapur and Lamberson, 1977).

For this work, the impact of the uncertainty associated with in-stream fecal coliform concentrations and mean annual streamflow in the Copano Bay watershed is explored. The analysis focuses only on nonpoint bacterial sources, as point sources likely show a different pattern. Therefore, Equation 4.1 simplifies to

$$L_f = \sum_{j=1}^{J} q_j c_j * e^{-k\tau_j} \tag{4.6}$$

Where: L_f = mean annual freshwater bacterial load (CFU/yr)

q_j = mean annual flow of water from nonpoint bacterial source j (m^3/yr)

c_j = expected mean concentration of bacteria from nonpoint source j (CFU/m^3)

k = first-order decay coefficient (yr^{-1})

τ_j = residence time from bacterial source *j* to modeled location (yr)

Results of the water quality sampling program described in Chapter 3 reveal a coefficient of variation (CV) of approximately 3 for fecal coliform concentrations, an average CV of 9 for streamflow at the watershed's main USGS gauge stations, and an average correlation of 0.5 between streamflow and fecal coliform concentrations at sites where both parameters were measured. (See Appendix D for more details.) This uncertainty analysis concentrates only on these CVs and assumes that they are reflective of the variance of the underlying population in the Copano Bay watershed. Since $s_x{}^2 = (CV_x * x)^2$, where $s_x{}^2$ is the variance of *x* and *x* is a random variable, the equation for variance in the freshwater loading of fecal coliform due to variance in concentrations and streamflow becomes

$$s_{L_f}{}^2 \approx \sum_{j=1}^{J}\left(\frac{dL_f}{dc_j}\right)^2\left(CV_{c_j} * c_j\right)^2 + \sum_{j=1}^{J}\left(\frac{dL_f}{dq_j}\right)^2\left(CV_{q_j} * q_j\right)^2 + 2 * \sum_{j=1}^{J}\left(\frac{dL_f}{dc_j}\right)\left(\frac{dL_f}{dq_j}\right)\rho_{c_j,q_j}\left(CV_{c_j} * c_j\right)\left(CV_{q_j} * q_j\right) \quad (4.7)$$

Where: ρ_{c_j,q_j} = coefficient of correlation between c_j and q_j

Similarly, variance in the bacterial loading in tidal rivers is calculated as

$$s_{L^*}{}^2 \approx \left(\frac{dL^*}{dL_f}\right)^2 s_{L_f}{}^2 + \left(\frac{dL^*}{dQ^*}\right)^2 \left(CV_{Q^*} * Q^*\right)^2 + 2\left(\frac{dL^*}{dL_f}\right)\left(\frac{dL^*}{dQ^*}\right)\rho_{L_f,Q^*} s_{L_f}\left(CV_{Q^*} * Q^*\right) \tag{4.8}$$

And the variance in the total loading to Copano Bay from tidal rivers and overland runoff is

$$s_{L_w}{}^2 \approx \left(\frac{dL_w}{dL_d}\right)^2 s_{L_d}{}^2 + \sum \left(\frac{dL_w}{dL^*}\right)^2 s_{L^*}{}^2 \tag{4.9}$$

Results of the First Order Analysis of Uncertainty at select locations are shown in Table 4.5.

Table 4.5: Results of First Order Analysis of Uncertainty for Nonpoint Source Loading

Modeled Variable	**Mean Annual Load (10^{15} CFU/yr)**	**St. Dev. in Modeled Load (10^{15} CFU/yr)**	**Coefficient of Variation**
Nonpoint Source Load from Aransas River Tidal to Copano Bay	0.66	4.15	6.30
Nonpoint Source Load from Mission River Tidal to Copano Bay	0.67	4.83	7.18
Nonpoint Source Load from Overland Flow Directly to Copano Bay	4.91	7.99	1.63
Overall Nonpoint Source Load from Watershed to Copano Bay	6.24	10.20	1.64

This analysis shows a portion of the uncertainty associated with modeling bacteria in natural systems. Results show a coefficient of variation in the overall watershed nonpoint source loading of fecal coliform to the bay of over one, implying a wide distribution about the modeled mean value and confirming the difficulty in accurately modeling bacteria in coastal systems. Though the uncertainty of the modeled mean annual nonpoint source loading to Copano Bay is large, the relative loading from each nonpoint bacterial source is assumed reflective of actual conditions (i.e., the ranking of the sources in Table 4.3 is assumed correct).

4.5 CONCLUSIONS FOR CHAPTER 4

TMDL Balance is a steady state, mass balance, GIS-based model for simulating pollutant loads and concentrations in coastal systems. The model was developed in the context of modeling bacterial TMDLs along the Texas Gulf Coast, but the approach is applicable to a wide variety of pollutants and geographic areas. Basing the model in GIS allows for the use of nationally accepted and widely available datasets. This reduces the effort needed to develop such data at the outset and also increases the transferability of the approach to watersheds outside of our particular study area.

This chapter presents the TMDL Balance model through a case study of mean annual bacterial loading conditions in the Copano Bay system. All available hydrology data was used in the model calibration; therefore, a validation of the calibrated model was not performed. The case study provides an example of distributing bacterial sources spatially based on land use data. The importance of this distribution is highlighted in the comparison of total loading results. Output shows that sources that contribute a large

portion of the overall bacterial load, but are located spatially distant from the bay, play a reduced role in the load of bacteria that eventually reaches Copano Bay under mean annual conditions. The importance of accurately locating a source's proximity to the impaired waterbody is highlighted. It is also noted, however, that Copano Bay is not violating water quality standards under mean annual conditions. Trends in bay bacterial concentrations point toward violations under high flow conditions when a larger percent of the load from spatially distant sources will reach the bay (due to a lower residence time in the river system resulting in less bacterial decay).

Using the first-order bacterial decay constant for model calibration allows the simulation of k values as mean annual net decay coefficients. Resulting decay values in the watershed varied spatially with values ranging from 1.91 $days^{-1}$ to 7.64 $days^{-1}$. Smaller decay coefficients are seen in the lower watershed, potentially implying regrowth and/or resuspension in these areas. The decay coefficient within Copano Bay was computed as 0.21 $days^{-1}$. While the calibration resulted in watershed decay coefficients that were in the expected range, the bay coefficient was among the minimum expected values reported in the literature. It is noted that literature values represent a pure decay coefficient, while the results of this analysis are a net decay that combines internal losses (i.e., die-off and grazing) and gains (i.e., resuspension and regrowth) into a single parameter. Therefore, the resulting bay k value of 0.21 $days^{-1}$ might indicate the presence of bacterial sources internal to Copano Bay, which are not explicitly accounted for in the modeling approach. Similarly, the pure decay coefficients in the watershed portion of the model might actually be higher than the net values that are computed in this work.

A First Order Analysis of Uncertainty illustrates the variability involved with modeling bacterial contamination in coastal systems, resulting in a coefficient of

variation of 1.6 when modeling the mean annual nonpoint source fecal coliform loading from the watershed to Copano Bay. This inherent uncertainty was a major factor when state and federal agencies recommended the development and use of simplified modeling approaches.

Chapter 5: Computing Mean Annual Maximum Loads in the Copano Bay System

5.1 INTRODUCTION

Twenty-seven of the forty-four bays on the Texas Gulf Coast are listed as impaired on the 2006 Texas List of Impaired Waters (TCEQ, 2007a). Twenty-one of those bays are listed for exceeding the bacterial water quality standard for oyster waters, which states that the median concentration of fecal coliform in the bay must be less than or equal to 14 colony forming units per one hundred milliliters [CFU/100ml] and that no more than 10% of samples can exceed 43 CFU/100ml (TNRCC, 2000). Similarly, twenty of the thirty-three Gulf Coast tidal river sections are considered impaired for contact recreation (TCEQ, 2007a). Twelve of these impairments are based on bacterial standards which state that the geometric mean concentration of enterococci must be less than or equal to 35 CFU/100ml and that no more than 25% of samples may exceed 89 enterococci CFU/100ml (TNRCC, 2000). The purpose of this work is to develop an approach to compute maximum mean annual bacterial loadings to coastal waterbodies, using historic data to translate these mean loadings to the concentration probabilities that the water quality criteria address.

The Copano Bay watershed is an example of a Texas Gulf Coast watershed with waterbodies that violate bacterial water quality standards. Typical of the coastal area, the Copano Bay watershed contains three types of waterbodies: freshwater rivers, tidal rivers, and bays. Modeling water quality in these systems is complex due to the interactions between the waterbodies and the impact of tidal hydraulics. This complexity might

require water quality models that describe two- or three-dimensional flow simulated on short time steps to accurately account for mixing and flushing scenarios. However, a recent State Task Force recommends the use of simple modeling techniques when simulating bacterial contamination in waterbodies on the List of Impaired Waters (Task Force, 2007). A less complex approach to modeling water quality in bays is provided by the steady state mass balance tidal prism approach (Ketchum, 1951). The tidal prism approach considers estuarine flushing as a function of freshwater inflows and tidal interactions over one or more tidal cycles. Waters that enter the estuary on the flood tide are assumed to be completely mixed and a portion of the water that escapes on the ebb tide returns on the following flood tide (Dyer, 1973; Fischer et al., 1979). A series of studies done by researchers at the Virginia Institute of Marine Science developed an approach using the tidal prism method for modeling bacterial TMDLs (Kuo and Neilson, 1988; Shen et al., 2005). This approach has been successfully used in bacterial TMDL studies in a number of bays along the Virginia Coast (Kuo et al., 2005; Virginia Department of Environmental Quality, 2005). A geographic information system (GIS)-based variant of this approach, the TMDL Balance model, is used here for TMDL analysis in the Copano Bay watershed.

This paper describes the bacterial water quality of the waterbodies in the Copano Bay watershed that violate bacterial water quality standards: the Mission Tidal River, the Aransas Tidal River, and Copano Bay. The TMDL Balance model is used to simulate bacterial loadings under mean annual conditions, modeling Copano Bay using the tidal prism approach. Historic water quality data are used to translate the modeled mean annual concentrations to the concentrations regulated by state water quality standards.

Model output is then used to compute the waterbodies' TMDLs under mean annual conditions and the required percent load reductions.

5.2 METHODS

5.2.1 Study Area

The Copano Bay watershed is located on the Texas Gulf Coast, as shown in Figure 5.1. Copano Bay is one of Texas's inner bays, located on the landward side of St. Joseph Island and interacting with Aransas Bay instead of directly with the Gulf of Mexico. The Copano Bay watershed is 5,620 km^2 in area and contains mainly rural land uses, with 94% of the watershed being classified as either agricultural, forest or rangeland (USGS, 2008). Four main waterbodies flow into Copano Bay: the Mission River, the Aransas River, Copano Creek, and Chiltipin Creek; however, TCEQ has historically only regulated water quality in the Aransas and Mission Rivers. The tidal portions of these rivers and Copano Bay are all listed as impaired for bacteria on the Texas List of Impaired Waters (TCEQ, 2007a). TMDL studies are currently underway for enterococci in the tidal rivers and fecal coliform in the bay.

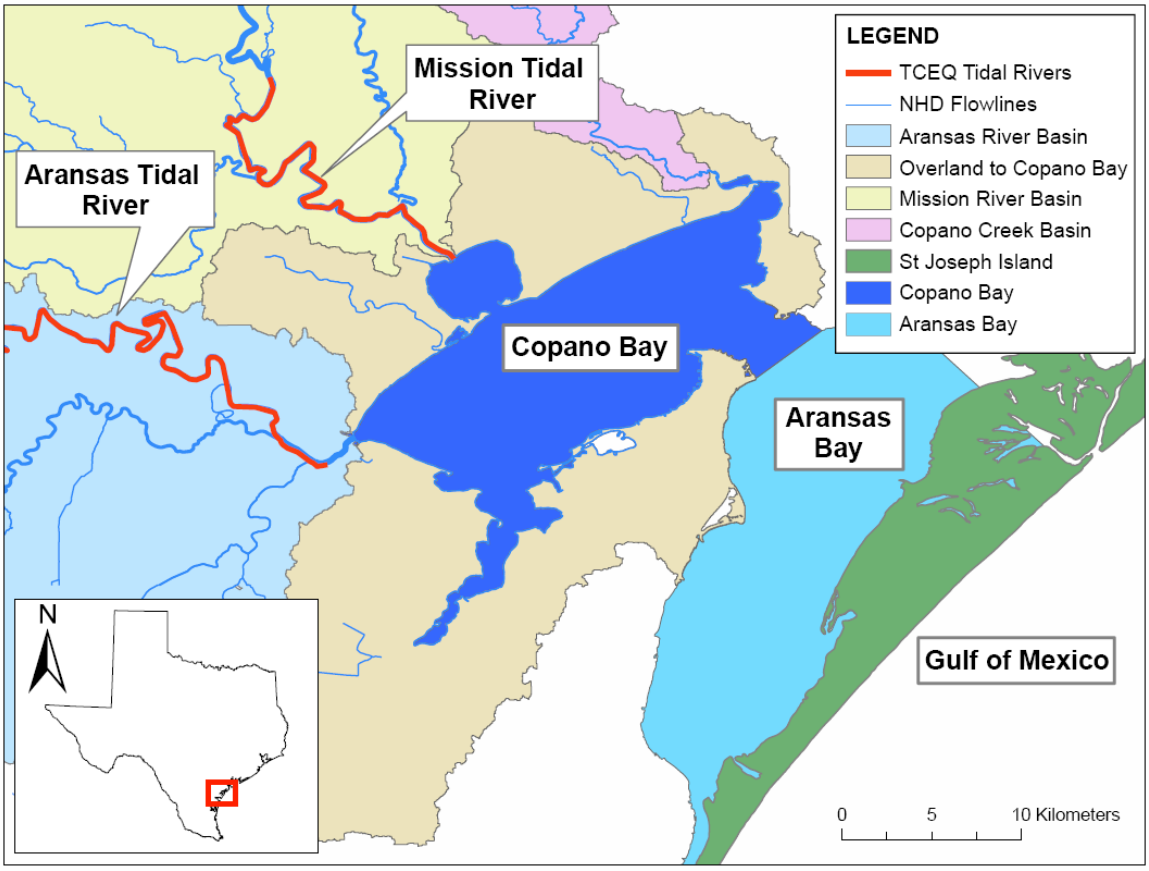


Figure 5.1: Copano Bay System

5.2.2 Data Sources

Watershed Data. The majority of geospatial data describing the drainage area around Copano Bay is obtained from the National Hydrography Dataset Plus (NHDPlus) (Horizon Systems, 2007). In addition to geospatial data such as flowlines and catchments, NHDPlus also includes estimates of value added attributes, which contain

data such as the mean annual precipitation and the fraction of a given land use in each watershed catchment.

Water Quality. The primary source of surface water quality monitoring (SWQM) data for this study is the TCEQ SWQM Information System (TCEQ, 2007c). Historic data on bacterial concentrations were obtained for the TCEQ water quality segments shown in Figure 5.1. Data collected by the Texas Parks and Wildlife Department (TPWD) over thirty years were also used to quantify historic salinity levels in Copano and Aransas Bays.

Tidal Waterbody Data. Historic data on water levels in the bays were obtained from the Texas Coastal Ocean Observation Network (TCOON) of Texas A&M University – Corpus Christi (TAMUCC, 2007). TCOON continuously monitors water levels at a station near the mouth of Copano Bay on 6-minute intervals. For this work, these data are assumed reflective of water levels in the bay as a whole. Values were combined with bay bathymetry data (Ward, 1997) and recently collected coastal LiDAR data (TNRIS, 2008) to calculate bay volumes and assess the extent of tidal influence.

5.3 BACTERIAL WATER QUALITY

5.3.1 Water Quality in the Tidal Rivers

Water quality is regulated in the Copano Bay watershed by calculating summary statistics for bacterial indicators at the TCEQ SWQM sites. Data collected in the Mission Tidal River between December 1999 and November 2006 (the most recent TMDL assessment period) shows that the 75% enterococci concentration value (the concentration that 75% of data points were less than) is 150 CFU/100ml. The geometric

mean of the concentrations is 67 CFU/100ml and the arithmetic mean is 266 CFU/100ml (TCEQ, 2008). These values are shown in Table 5.1 along with the summary statistics computed for the Aransas Tidal River segment.

Table 5.1: Summary Statistics of Bacterial Water Quality in Tidal Rivers (December 1999 – November 2006)

Waterbody	75% Value	Geometric Mean	Arithmetic Mean
Mission Tidal River (enterococci CFU/100ml)	150	67	266
Aransas Tidal River (enterococci CFU/100ml)	590	115	908

The results shown in Table 5.1 indicate that the Mission and Aransas Tidal River segments violate water quality standards under both the geometric mean and 75% concentration (i.e., the concentration that 75% of samples are less than or equal to or that 25% of samples exceed) criteria (this is also noted on Figure 5.2). The data also show that the bacterial concentrations are log-normally distributed, which is typical of bacterial concentrations in natural systems (McBride, 2005). Figure 5.2 shows the seven years of Mission Tidal River enterococci concentrations on a log-transformed normal probability plot. Note that these data fit the log-normal distribution well for all but the largest concentrations.

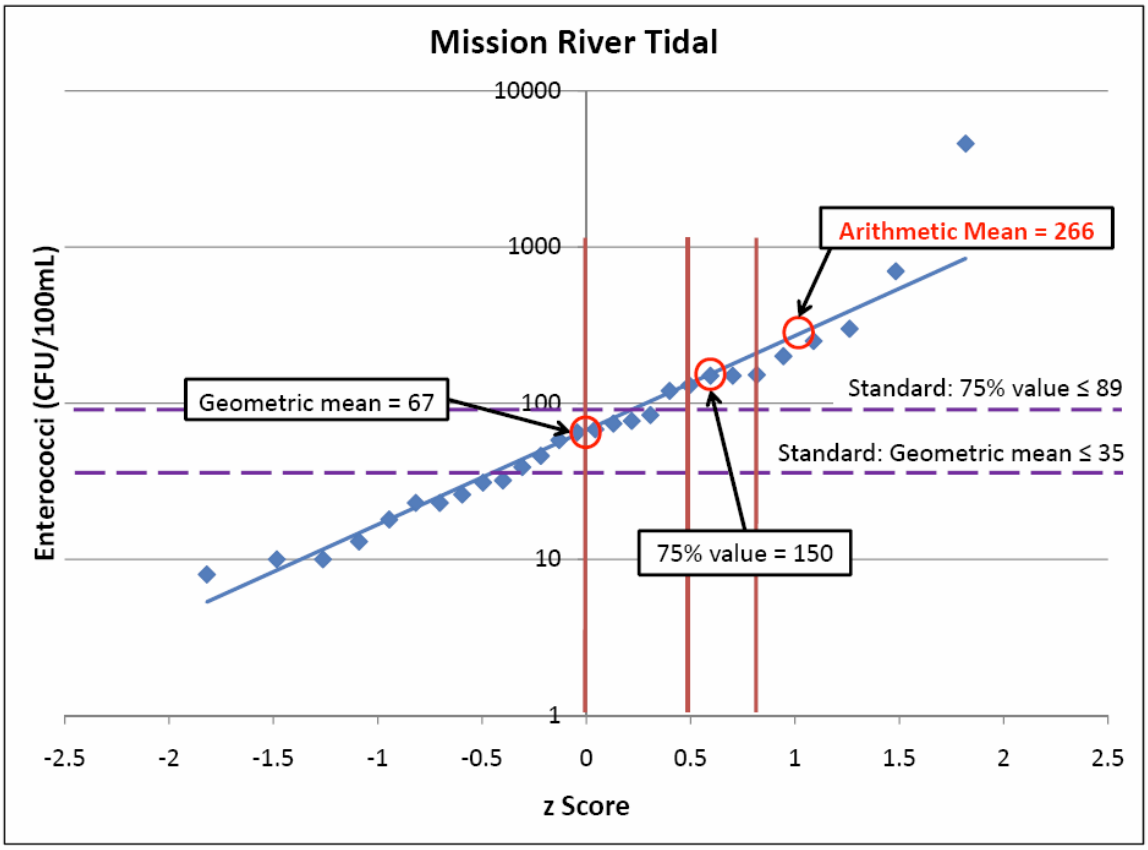


Figure 5.2: Bacterial Water Quality in Mission Tidal River

5.3.2 Water Quality in Copano Bay

Under Texas water quality standards, Copano Bay's water quality is regulated to protect oyster harvesting. Bays classified as oyster waters have water quality criteria that use fecal coliform as the bacterial indicator and address the median concentration and the concentration that no more than 10% of samples exceed. Water quality in Copano Bay is regulated by sampling sixteen sites within the bay, which are shown in Figure 5.3. The

median concentration at each of these sites must be ≤ 14 CFU/100ml and 90% of the samples at each site must be ≤ 43 CFU/100ml (TNRCC, 2000).

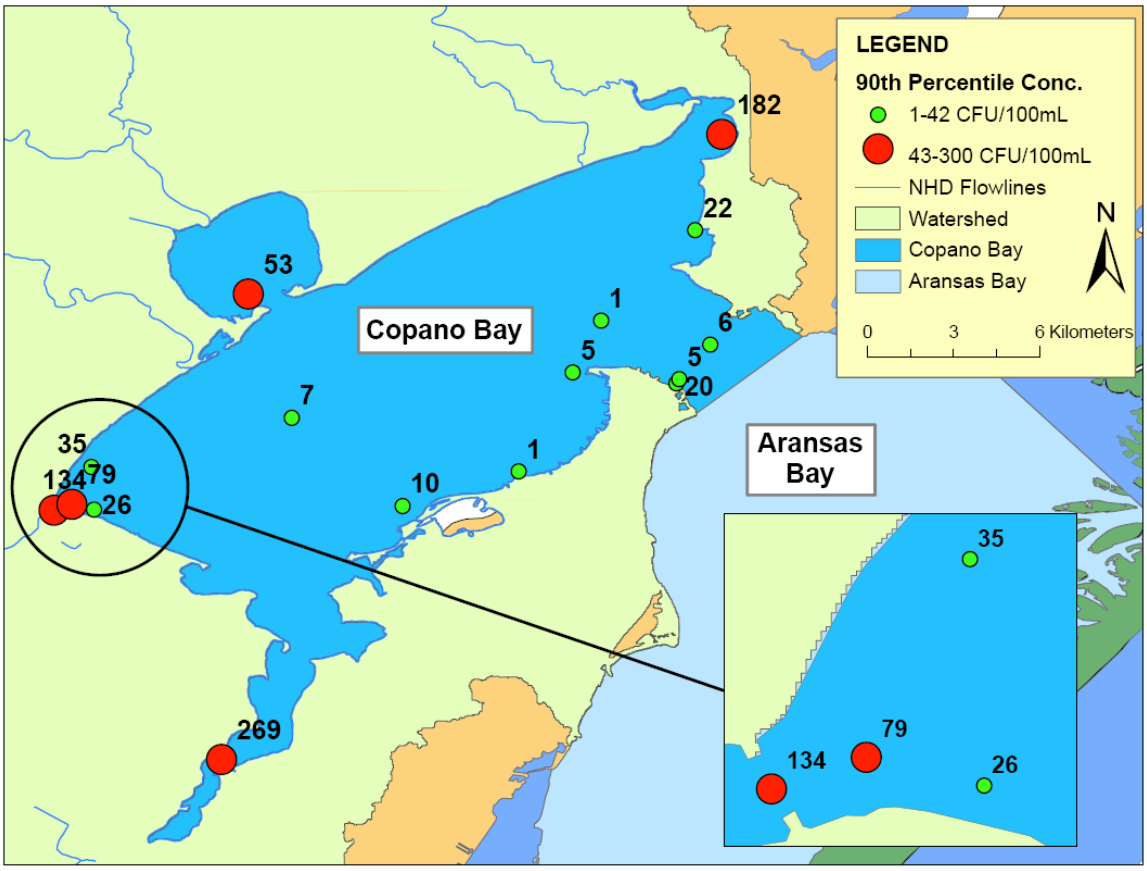


Figure 5.3: 90th Percentile Fecal Coliform Concentration at SWQM Sites in Copano Bay

Statistics were computed for each of the Copano Bay sites using 638 samples that were collected during the most recent seven year TMDL assessment period (December 1999 to November 2006) (TCEQ, 2008). Figure 5.3 denotes each site by its estimated 90th percentile fecal coliform concentration (computed using the "robust" regression on

order statistics approach and assuming that the 90th percentile is reflective of the 90% concentration, as discussed below) showing that five of the sites violate under this criterion (i.e., the concentration that 90% of samples are less than is greater than 43 CFU/100ml). All sites meet the median concentration water quality criterion. The five violating sites in Copano Bay are all located in parts of the bay where watershed loading is the primary source of bacteria. These locations are also hydraulically distant from tidal interactions with Aransas Bay.

Computing the summary statistics for the Copano Bay fecal coliform data posed a challenge since 73% of the reported values are below the laboratory's detection limit (i.e., censored), which was generally 2 CFU/100ml. Other common detection limits in the data included 1, 3, and 10 CFU/100ml. One common approach to computing statistics for censored data is to replace the censored data points with an arbitrary number, such as half of the detection limit. However, this is undesirable as it does not give a representative understanding of what is occurring with concentrations that are less than can currently be detected and has the potential to produce misleading statistics. For example, if the substitution approach was used with the Copano Bay fecal coliform data, over 70% of the concentrations would be reported as 1 CFU/100ml, leading to a median value of 1 CFU/100ml.

Another approach for analyzing censored data is the "robust" regression on order statistics method ("robust" ROS) (Helsel, 2005). "Robust" ROS assumes that if censored data were able to be detected they would follow the same distribution as those values that were actually measured. Since bacterial concentrations typically follow a log-normal distribution (McBride, 2005), as shown in the tidal river segments, the detected bacterial concentrations are log-transformed to perform this analysis. The transformed data are

placed on a probability plot and a regression line is fit. It is assumed that data below the detection limit follow this same regressed distribution and one can predict each censored data value based on the z-score of the data point (Helsel, 2005). Predicted values are then combined with the detected values and used to compute the summary statistics of the distribution. Transformation bias is avoided by transforming each data point back to its original units (i.e., from ln[CFU/100ml] to CFU/100ml) before the summary statistics are computed (Helsel, 2005).

Figure 5.4 shows the result of "robust" ROS analysis for the seven years of fecal coliform data at TCEQ Site 14797. The fitted distribution can be used to estimate the concentration that no more than 10% of samples values exceed (i.e., the 90^{th} percentile). This value is indicated on Figure 5.4, which shows that Site 14797 violates the fecal coliform water quality standard at this metric (as was pointed out in Figure 5.3). The site is in compliance under the median condition.

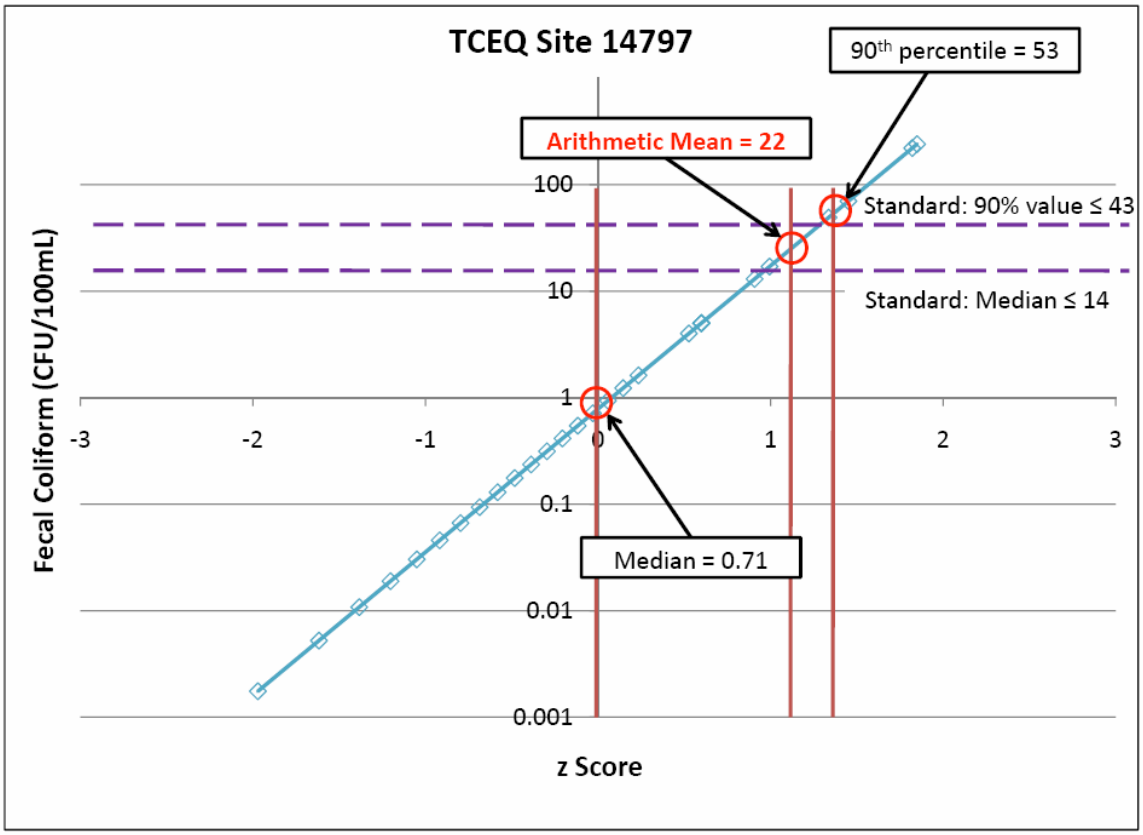


Figure 5.4: "Robust" ROS Analysis for Fecal Coliform at TCEQ Site 14797

Figure 5.5 shows the result of "robust" ROS analysis for each of the five TCEQ sites that are violating the fecal coliform water quality standards (Figure 5.3) and also for the analysis performed when modeling Copano Bay as a single waterbody (i.e., calculating the statistics by grouping all of the Copano Bay water quality data together). Results for modeling Copano Bay as a single waterbody show an arithmetic mean concentration of 24 CFU/100ml, a median of 0.5 CFU/100ml, and a 90th percentile of 22

CFU/100ml. Therefore, when modeling Copano Bay as a single waterbody the water quality standards are met. This is discussed further in Section 5.4.2.

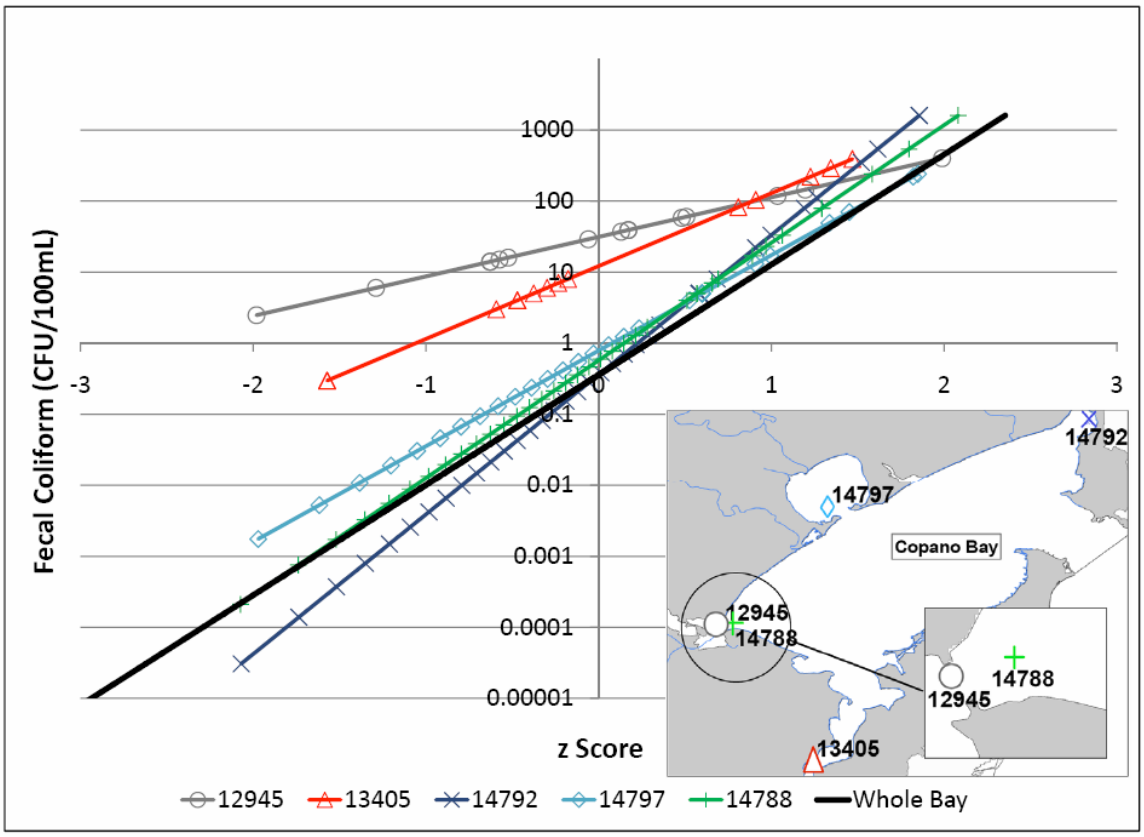


Figure 5.5: "Robust" ROS Analysis for Copano Bay at Violating Sites and Whole Bay

5.4 Computing the Allowable Bacteria Concentrations

To bring the Mission Tidal River, Aransas Tidal River, and Copano Bay back into compliance with bacterial water quality standards, the TMDL Balance model (presented

in Chapter 4) was used to compute the load of bacteria that can enter each segment while still meeting the water quality standards. Since the TMDL Balance model simulates mean conditions and the bacterial water quality standards are written to address the concentration under geometric mean or median and 75% or 90% conditions, an approach is presented to convert between these concentrations. In the case of Copano Bay, a relationship is also developed between the bacterial concentration in the bay when modeled as a single waterbody and the concentrations at each violating water quality site in the bay.

5.4.1 Concentrations in the Tidal Rivers

Consider the enterococci concentrations in the Mission Tidal River segment as shown in Figure 5.2. It is first assumed that the historic relationship (i.e., the slope of the distribution, which also represents the standard deviation of the logarithms of the data) between the arithmetic mean, geometric mean, and 75% value is constant. As shown in Figure 5.6, reducing the arithmetic mean concentration of enterococci (moving the distribution down on the graph) also reduces the geometric mean and 75% concentration. To compute the permissible concentrations in this segment, the arithmetic mean concentration is reduced until the correlated geometric mean and 75% concentrations meet the water quality standard, resulting in an allowable arithmetic mean concentration of 137 CFU/100ml. Note that, in this case, the geometric mean value controls the magnitude of the reduction.

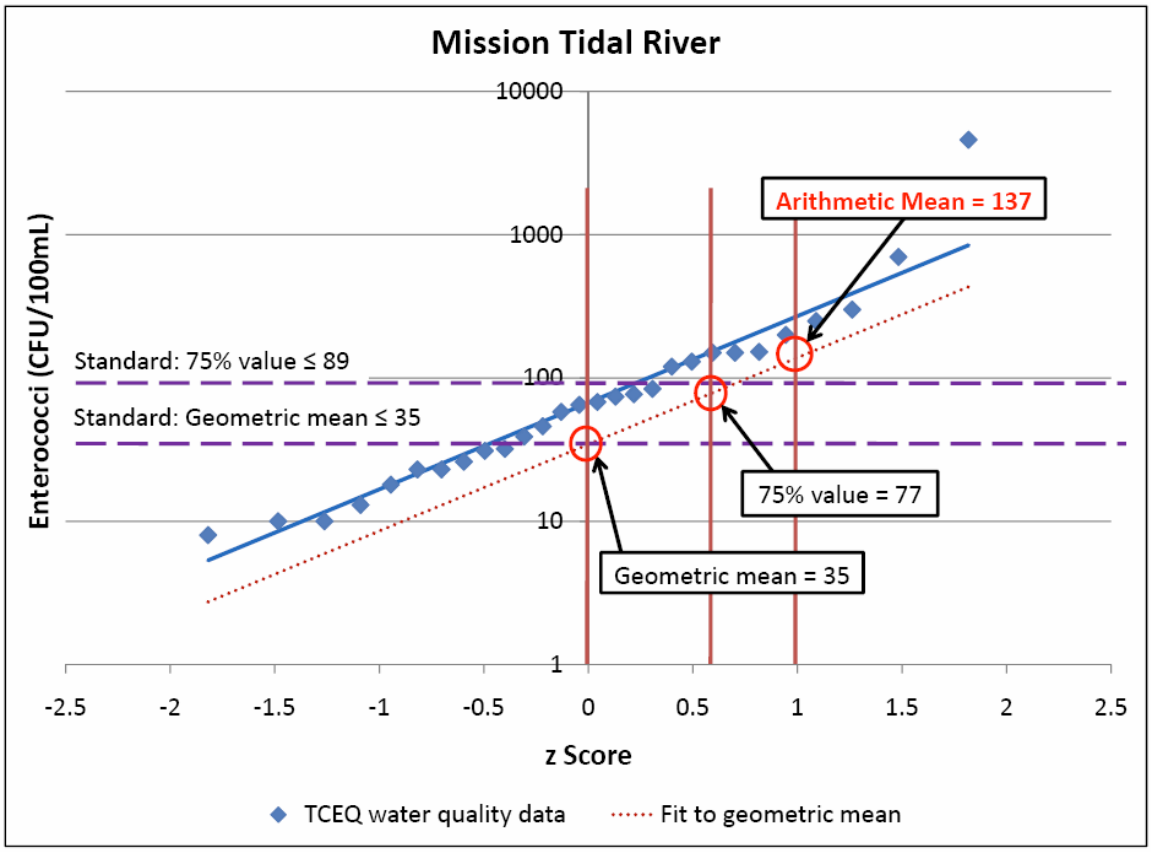


Figure 5.6: Permissible Concentrations of Enterococci in the Mission Tidal River

A similar computation is done for the Aransas Tidal River, as shown in Figure 5.7. In this case, the 75% concentration controls the magnitude of the reduction. The allowable arithmetic mean concentration is 137 enterococci CFU/100ml.

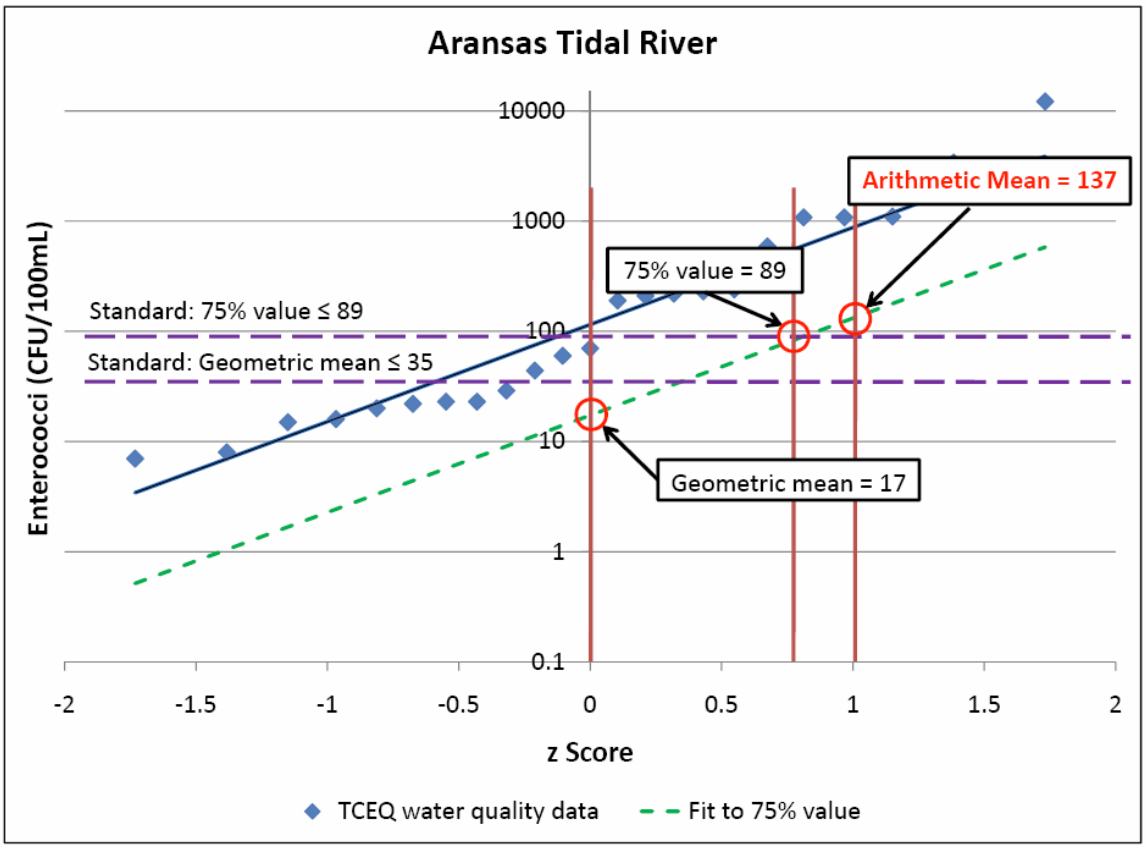


Figure 5.7: Permissible Concentrations of Enterococci in the Aransas Tidal River

As described in Chapter 4, the TMDL Balance model is developed to simulate the loading and concentrations of fecal coliform. Therefore, to address the water quality in the tidal rivers the allowable enterococci concentrations must be converted to allowable fecal coliform concentrations, which can be used in the model. This task was achieved by using the relationship between the ln-transformed in-stream concentrations of the two indicator organisms, which was developed in Section 3.3.3. Table 5.2 summarizes the results.

Table 5.2: Permissible (Modeled) Bacterial Concentrations in the Tidal Rivers

Tidal River Segment	Allowable Enterococci Concentration (CFU/100ml)	Allowable Fecal Coliform Concentration (CFU/100ml)
Mission	137	23.6
Aransas	137	23.6

5.4.2 Concentrations in Copano Bay

Performing this analysis for Copano Bay is slightly more complex. As shown in Figure 5.5, when modeled as a single waterbody, Copano Bay is not violating the fecal coliform water quality standards. When considered at each individual site, however, there are five locations that violate the standard. Since TMDL Balance simulates Copano Bay as a single waterbody, a relationship is needed between the bacterial concentrations at each individual site and those for the bay as a whole to compute the permissible arithmetic mean fecal coliform concentration in Copano Bay.

The first assumption made in this analysis is that each station's contribution of bacteria to the overall distribution of the bay will remain constant as the bacterial concentrations increase or decrease. In practice, this means that if the bacterial concentration at a site has historically been twice that in the bay as a whole, as bacterial concentrations are reduced the site in question will continue to experience concentrations that are twice as large as the bay as a whole. Using the same approach presented in Section 5.4.1, where the relationship between the arithmetic mean, geometric mean, and upper percentile (in this case, the 90% value) remains the same, the mean fecal coliform concentration in Copano Bay is reduced. Reducing the overall concentration then reduces the concentrations at each individual site. The values are all reduced until the most polluted site meets the median and 90% water quality criteria (modeled as the 90th

percentile concentration in this approach). The resulting arithmetic mean concentration within Copano Bay as a whole is 3.7 CFU/100ml, as shown in Table 5.3 and Figure 5.8. The controlling scenario, in this case, is Site 13405 at the 90th percentile concentration. The regulated concentrations at Site 13405 are labeled in Figure 5.8.

Table 5.3: Permissible (Modeled) Concentrations of Fecal Coliform within Copano Bay

Site	**Median (CFU/100ml)**	**90th Percentile (CFU/100ml)**	**Arithmetic Mean (CFU/100ml)**
12945	5.0	21.3	10.5
13405	1.9	42.7	12.7
14792	0.06	28.9	18.3
14797	0.12	8.4	3.5
14788	0.09	12.5	11.1
Whole Bay	0.08	3.5	3.7

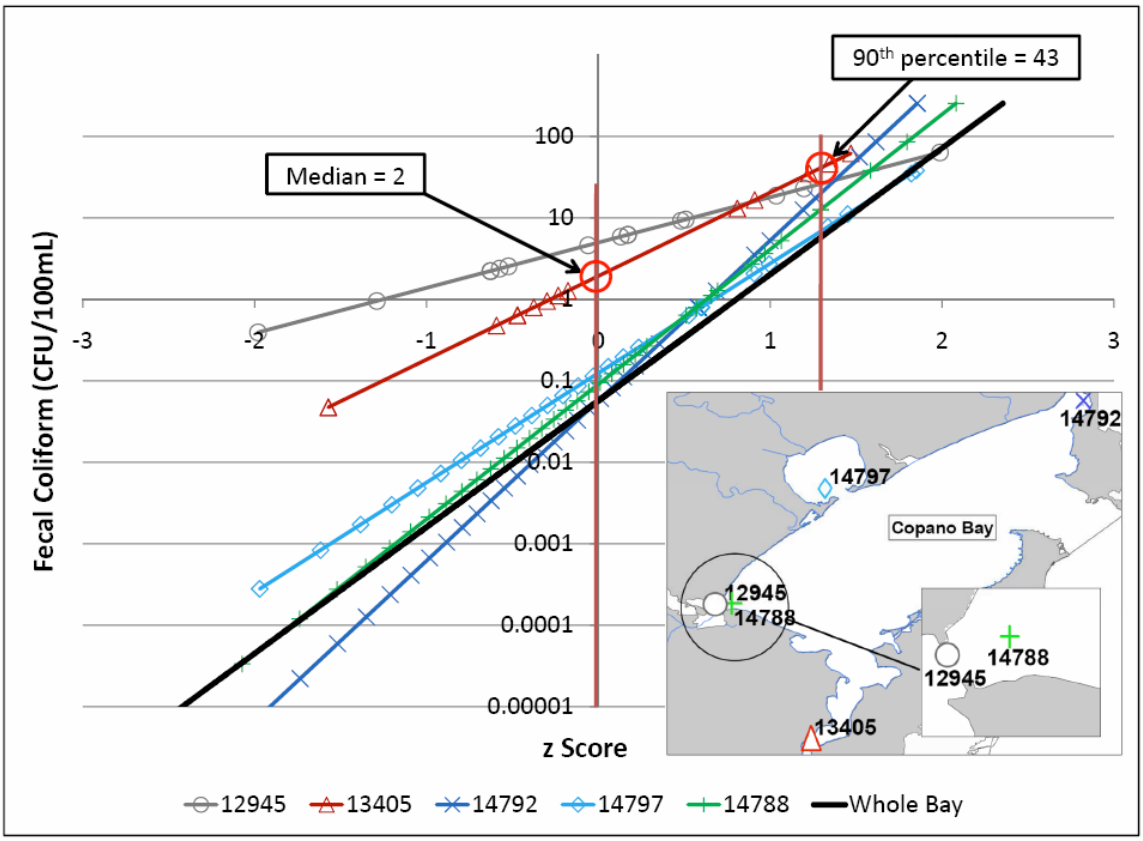


Figure 5.8: Permissible Concentrations of Fecal Coliform in Copano Bay

5.5 Computing the Tidal River TMDLs

To calculate the mean annual TMDL (i.e., the total maximum daily load that can be contributed to the waterbody under mean annual conditions) in the tidal river segments, results of the analysis in Section 5.4 are combined with results from the TMDL Balance model under mean annual conditions. Calculations were performed such that the allowable mean concentration is achieved at the tidal river SWQM site within each tidal

river. See Figure 5.9 for an explanation of this concept using the Mission Tidal River SWQM Site 12943 as an example.

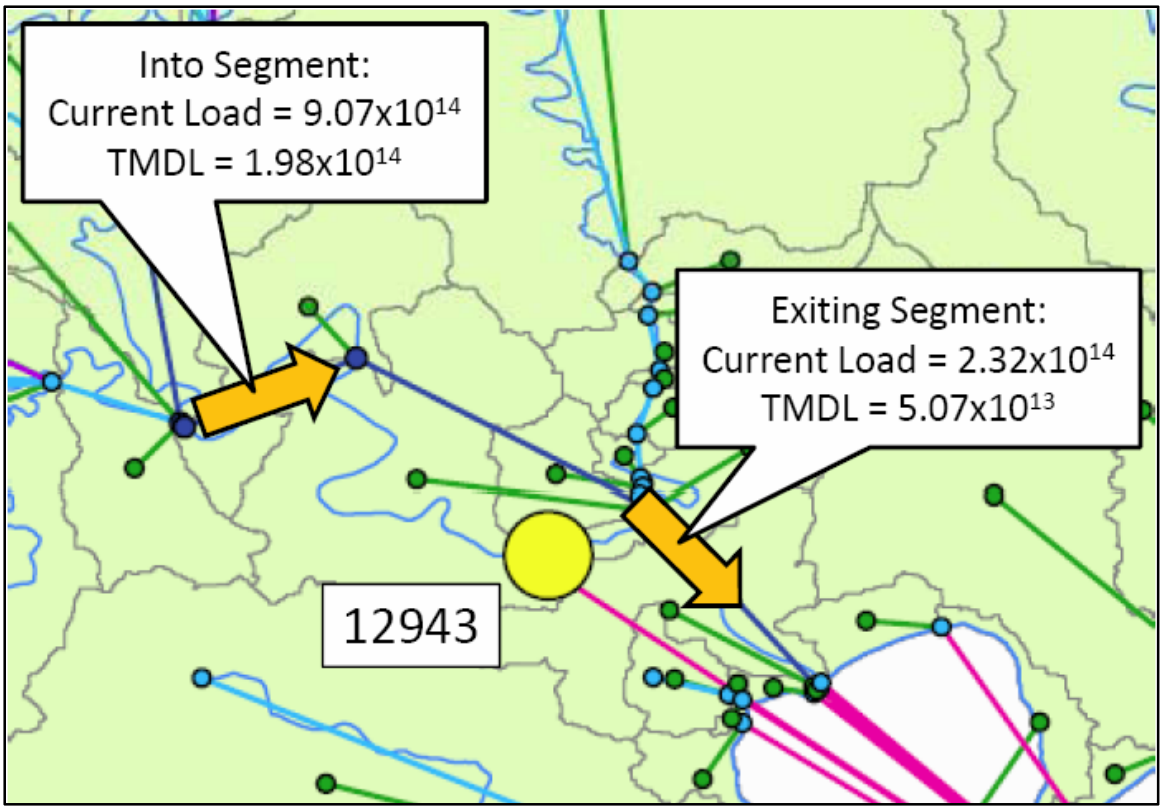


Figure 5.9: Modeled Fecal Coliform TMDL at TCEQ SWQM Site 12943

Figure 5.9 shows the TMDL Balance schematic network in the area of the Mission Tidal River, centered on the SchemaLink that represents the portion of the river where SWQM Site 12943 is located. To compute the TMDL for this river, the model was used to simulate the conditions under which the concentration of fecal coliform leaving the SchemaLink would be less than or equal to the allowable concentration of

23.6 CFU/100ml (which equates to a loading of $5.07x10^{13}$ CFU/yr under mean annual conditions). Keeping all other modeling parameters constant, this results in a mean annual TMDL into this river segment of $1.98x10^{14}$ CFU/yr. As shown in Figure 5.9, it is estimated that the current fecal coliform load to the segment is $9.07x10^{14}$ CFU/yr, so the TMDL represents a 78% reduction in loading.

A similar analysis was performed for the Aransas Tidal River. Note, however, that this river has two TCEQ SWQM sites associated with it, Sites 12948 and 12947. Since the majority of water quality data used in this work is from Site 12948 (because it has more monitoring data), the TMDL calculation was performed around the SchemaLink that contains that site. Results show a mean annual TMDL of $4.11x10^{14}$ CFU/yr of fecal coliform into the segment. With a current modeled load of $6.89x10^{15}$ CFU/yr, a 94% load reduction is needed.

5.6 COMPUTING THE COPANO BAY TMDL

5.6.1 Modeling Copano Bay

Before the TMDL calculation for Copano Bay is discussed, the modeling approach taken within the bay is presented. The bay's hydrologic processes under mean annual conditions are also presented to give insight to the impact that they have on water quality.

Tidal Prism Approach. The concentration of bacteria within Copano Bay is modeled using the tidal prism approach, shown in Equation 5.1. Using this approach, the concentration is a result of loading from the watershed, tidal interactions with adjacent waterbodies, and a first-order bacterial decay over one or more tidal cycles.

$$C = \frac{L_w + Q_a C_a}{(Q_{net} + Q_a) + kV} \quad (5.1)$$

Where: C = mean bacteria concentration in Copano Bay (CFU/m^3)

L_w = mean annual bacterial load to Copano Bay from the watershed (CFU/yr)

Q_a = mean annual quantity of water entering Copano Bay from Aransas Bay on the flood tide that did not exit Copano Bay on the previous ebb tide (m^3/yr)

C_a = mean pollutant concentration in Aransas Bay (CFU/m^3)

Q_{net} = mean annual net quantity of water exiting Copano Bay to Aransas Bay (m^3/yr)

k = first-order bacterial decay coefficient ($years^{-1}$)

V = mean annual volume of Copano Bay (m^3)

Water Balance. The first step in understanding the hydrology of Copano Bay is to develop a water balance under mean annual conditions. Figure 5.10 shows the water movement in and out of Copano Bay, ignoring groundwater interactions. The sources of water to Copano Bay are freshwater from the watershed, precipitation directly onto the bay, and water entering the bay on the flood tide from Aransas Bay. Water escapes Copano Bay through evaporation or as flow into Aransas Bay on the ebb tide. The net advective flow from Copano to Aransas Bay over the year is then the difference between the total inflow, outflow, and atmospheric interaction as summarized in Equation 5.2.

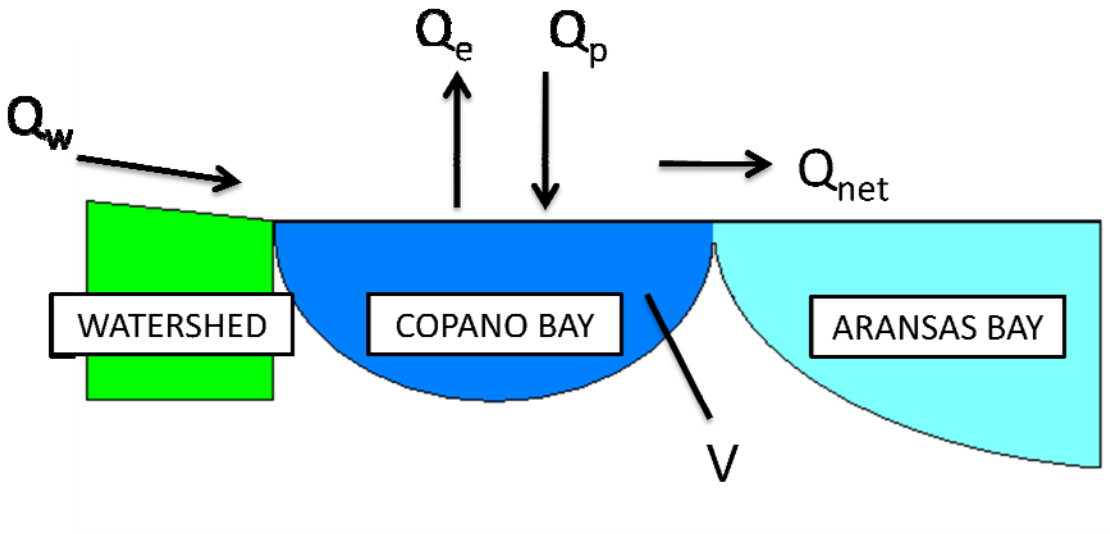


Figure 5.10: Water Balance on Copano Bay

$$dV/dt = Q_w + Q_p - Q_e - Q_{net} \quad (5.2)$$

Where: V = mean annual volume of the bay (m^3)

t = time step (year)

Q_w = mean annual quantity of water entering Copano Bay from the watershed (m^3/yr)

Q_p = mean annual quantity of water entering Copano Bay from precipitation (m^3/yr)

Q_e = mean annual quantity of water exiting Copano Bay through evaporation (m^3/yr)

Q_{net} = mean annual net quantity of water exiting Copano Bay to Aransas Bay (m^3/yr)

To understand the change in bay volume over time, historic water level data from the Texas Coastal Oceanic Observation Network (TCOON) were used to quantify the change in mean annual volume over the whole period of record (from 1993-2007). Water levels were converted to volumes using bathymetric data, revealing a mean annual change in volume of 1.1×10^6 m^3/yr, as shown in Table 5.4. Note that, when compared to the annual net movement of water through the bay (computed below at 539×10^6 m^3/yr), the magnitude of change in annual volume is insignificant. This permits an assumption of steady state conditions in the bay, which implies that Equation 5.2 is equal to zero and $Q_{net} = Q_w + Q_p - Q_e$.

Table 5.4: Mean Annual Water Balance on Copano Bay

Component	**Mean (10^6 m^3/yr)**
$\Delta V/\Delta t$	1.1
Q_w	637
Q_p	188
Q_e	286
Q_{net}	539

The volume of freshwater entering Copano Bay was computed as a function of the land use/land cover and precipitation in the watershed and the volume of effluent discharged by point sources, as discussed in Chapter 4 and Appendix B. The volume of water entering/exiting the bay from the atmosphere was calculated by combining the average precipitation/evaporation rates over the bay with the average bay surface area. According to NHDPlus, the weighted mean average precipitation in the catchments

immediately adjacent to Copano Bay is 890 mm/yr (Horizon Systems, 2007). The Texas Water Development Board (TWDB) estimates the mean annual open water evaporation in this area at 1,350 mm/yr (TWDB, 2008). The bay's surface area was estimated with historic TCOON water levels and bathymetric data resulting in a mean annual value of 237×10^6 m^2. Table 5.4 summarizes the mean annual water balance on Copano Bay, showing that, on average, the bay is losing water to the atmosphere through evaporation at the rate of 0.98×10^6 m^3/yr.

Referring to Equation 5.2, the net amount of water moving from Copano to Aransas Bay under mean annual conditions is 539×10^6 m^3/yr. This result shows that the Copano Bay system is mainly horizontally controlled. The majority of water that enters the bay exits into Aransas Bay.

Water Exchange between the Bays. While the results of the annual water balance on Copano Bay are insightful for a general understanding of the bay's hydrology, they are not sufficient for modeling water quality in the bay. For these purposes the net flow between Copano Bay and Aransas Bay must be dissected into individual components of inflow and outflow due to tidal movement and dispersion.

Figure 5.11 represents the movement of water from Copano Bay to Aransas Bay (denoted on left side of the figure) and from Aransas Bay back into Copano Bay (on the right side of the figure). Note that the bottom portion of the figure shows a volume of water that is denoted as Q_s. A portion of the water that moves between the bays during each tidal cycle is recycled, simply sloshing back and forth between Copano Bay and Aransas Bay. As this water moves from Copano Bay into Aransas Bay on the ebb tide and back into Copano Bay on the flood tide, it retains the properties of Copano Bay

water. Therefore, this recycled water is not of concern when modeling water quality because it has the same water quality characteristics as the water already in Copano Bay. Only the amount of "new" water that moves from Aransas Bay into Copano Bay is of concern, as this is the only water that actually changes the water quality in Copano Bay.

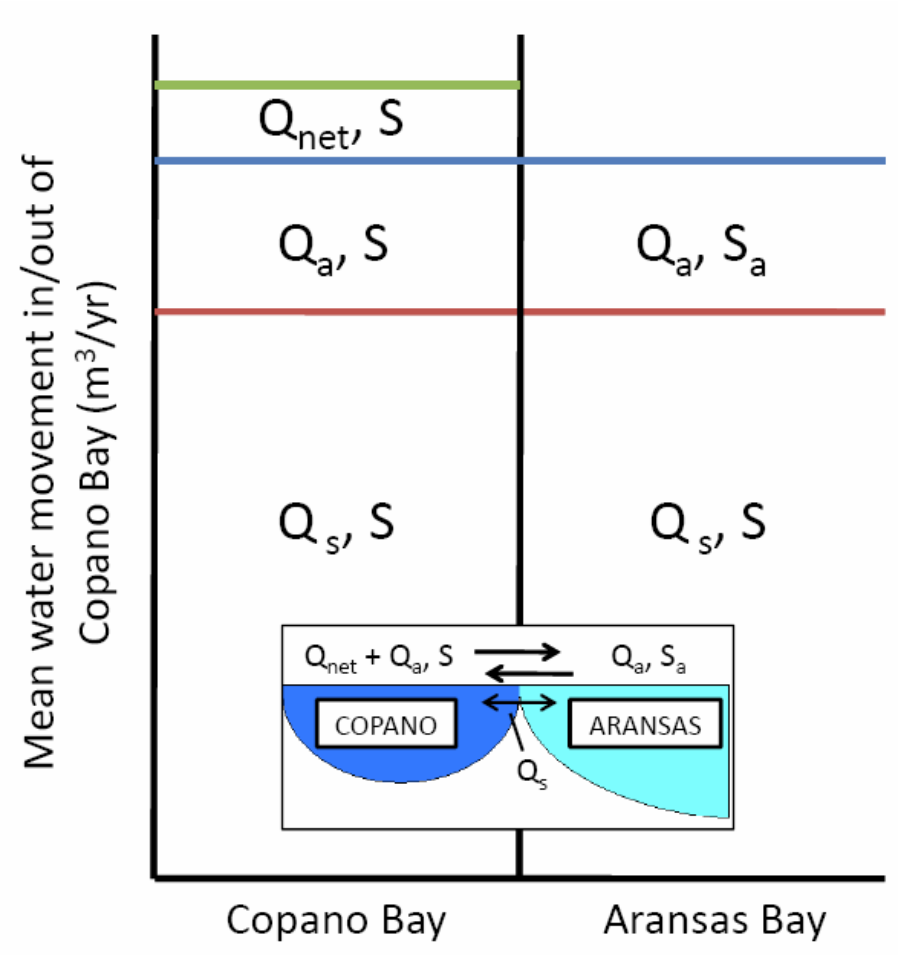


Figure 5.11: Exchange between Copano Bay and Aransas Bay and Associated Salinities

To separate the components of flow between the bays, salt was used as a tracer, tracking its movement in the system. Assuming the water entering Copano Bay from the watershed and from the atmosphere is fresh (i.e., salinity is zero) and ignoring the minor amount of salinity that's found in the tidal river waters (which averages around 1 ppt), the only source of salinity for Copano Bay is from Aransas Bay. This is shown through a balance of salinity in the Copano Bay system under steady state conditions as

$$(Q_a S_a + Q_s S) = (Q_s + Q_a + Q_{net})S \tag{5.3}$$

Where: Q_a = mean annual quantity of water entering Copano Bay from Aransas Bay on the flood tide that did not exit Copano Bay on the previous ebb tide (m^3/yr)

S_a = mean salinity in Aransas Bay water (ppt)

Q_s = mean annual quantity of water that sloshes back and forth between Copano Bay and Aransas Bay (m^3/yr)

S = mean salinity in Copano Bay water (ppt)

Equation 5.3 is re-arranged to solve for the amount of "new" Aransas Bay water entering Copano Bay as

$$Q_a = \left(\frac{S}{S_a - S}\right) Q_{net} \tag{5.4}$$

Salinity data from over thirty years of sampling by the TPWD was used to quantify the salinity in Copano and Aransas Bays. TPWD samples were collected on a wide spatial distribution while performing four different types of sampling procedures: gill nets, bag seines, oyster dredges, and trawls. To most effectively use the salinity data

as a tracer for water movement values that were collected during gill net and bag seine studies were disregarded, as they are more susceptible to shoreline activities and potentially less reflective of the salinity in outer bay waters. Salinity samples were also grouped into different zones in the bays to separate the samples from the interior of the bays from those collected near the mouth of Copano Bay, where mixing of the bay waters takes place. Basic statistics were calculated on the salinity in each zone to determine if any quantitative differences were present. As expected, the segments interior to Copano Bay had the smallest mean salinity value, those interior to Aransas Bay had the largest value, and the segments near the mouth had an intermediate value. To ensure that the analysis accounted for the salinity of purely Copano water and purely Aransas water while using the most data possible, the analysis was grouped into three general zones: Copano Bay, mixed zone, and Aransas Bay as shown in Figure 5.12. The mean salinity within these zones was calculated as 17 ppt in Copano Bay, 20 ppt in the mixed zone, and 24 ppt in Aransas Bay.

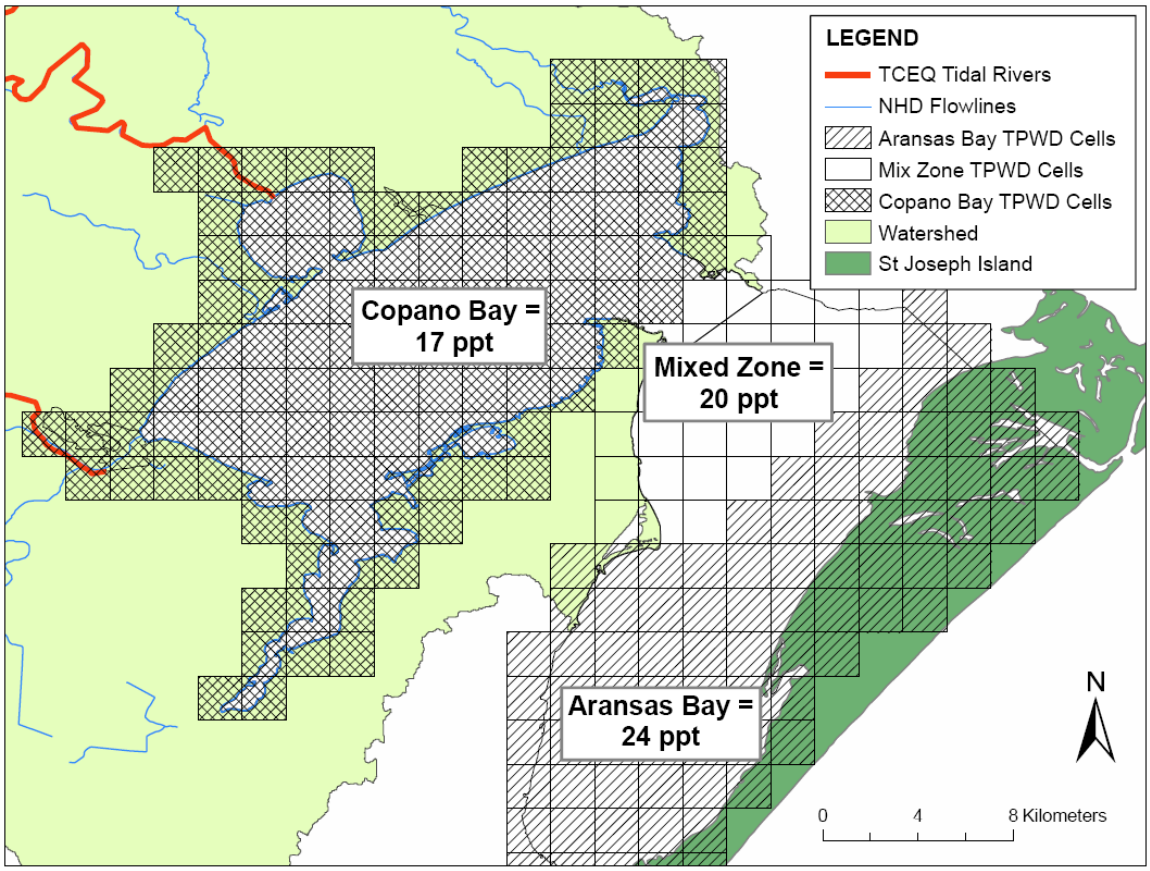


Figure 5.12: Mean Salinity Values in Copano Bay and Aransas Bay

The pattern of salinity in Figure 5.12 gives a qualitative understanding of the exchange of water between the watershed, Copano Bay, and Aransas Bay. As mentioned, the only source of salinity (for the purposes of this study) to Copano Bay is from Aransas Bay. The fact that Copano Bay has a salinity value greater than zero, therefore, indicates that water moves from Aransas Bay back into Copano Bay. The relative strength of the salinity in Copano Bay indicates that this water movement must be quite substantial. Equation 5.4 was used to quantify this movement by combining the

salinity values with the computed flows. Results show that the mean annual quantity of "new" Aransas Bay water entering Copano Bay is 1310×10^6 m^3/yr. Comparing this result with Table 5.5 shows that it is more than twice the quantity of water that enters from the watershed.

The impact of this tidal exchange is substantial when considering water quality. Figure 5.3 shows the 90^{th} percentile fecal coliform concentration at each of the 17 SWQM sites in Copano Bay. As noted, the sites with values that violate the water quality standard are located nearest to the shoreline. Those sites that are in the middle of the bay or near the mouth have very low concentrations. Noting that the bacterial concentration in Aransas Bay is low (discussed below) and that from the watershed is relatively high, implications of the mixing of Aransas waters into Copano Bay are seen. The low bacteria, high salinity Aransas Bay water reduces the bacterial concentrations and increases the salinity in those areas of Copano Bay that are subjected to mixing. One potential factor in the violating SWQM sites being near the shoreline is that they might be subject to less of this tidal mixing.

Movement of the "new" Aransas water is shown in the bacteria water quality balance in Figure 5.13. The balance was developed to account for bacterial loading from Aransas Bay and inputs from the watershed. Losses include loading to Aransas Bay and bacterial decay within Copano Bay.

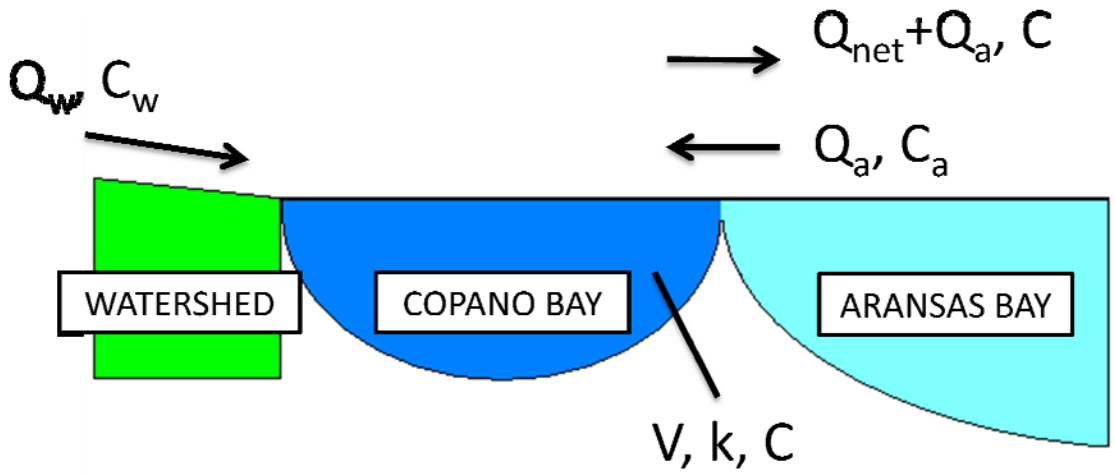


Figure 5.13: Bacteria Water Quality Balance on Copano Bay

The bacteria water quality balance under steady state mean annual conditions is written as

$$Q_w C_w + Q_a C_a - (Q_{net} + Q_a)C - kVC = 0 \quad (5.5)$$

Where: C_w = mean concentration of bacteria in water exiting the watershed (CFU/m^3)

k = first-order decay coefficient ($years^{-1}$)

Note that Equation 5.5 neglects groundwater and atmospheric exchange as sources or sinks of bacteria. It also neglects the internal loading of bacteria to the system (i.e., bacterial regrowth or resuspension from the sediments). Though other work has shown that sediments can act as a reservoir for bacteria (Erkenbrecher, 1981; Goyal et al.,

1977; Matson et al., 1978; Shiaris et al., 1987; Valiela et al., 1991) and could potentially be a source of bacteria to systems such as these (Jamieson et al., 2003), there are rarely sufficient data available to characterize the sediment bacterial load. To acknowledge the exclusion of internal loading and groundwater interactions in the TMDL Balance model, the first-order decay coefficient is used as a calibration parameter in the modeling approach. The coefficient then becomes a net decay coefficient, signifying both losses and gains internal to the bay. This topic is addressed in Section 4.4.3 where the net decay coefficient is computed as 0.21 $days^{-1}$. Rearranging Equation 5.5 to solve for the mean annual concentration of bacteria in Copano Bay, results in the tidal prism equation (Equation 5.1), where $Q_w C_w = L_w$. The TMDL Balance model combines the result of Equation 5.1 with the quantity of water exiting Copano Bay to Aransas Bay that does not return on the following tide ($Q_{net} + Q_a$) to compute the total load of fecal coliform exiting Copano Bay to Aransas Bay.

5.6.2 Computing the TMDL

The fecal coliform TMDL for Copano Bay is computed using a similar approach to that taken in the tidal river segments. Since the water entering Copano Bay from Aransas Bay serves to dilute the bacterial concentrations within Copano Bay, the necessary load reduction to Copano Bay is simulated solely as a reduction in loading from the watershed. The current load of fecal coliform entering Copano Bay from the watershed is modeled at 7.65×10^{15} CFU/yr (see Table 4.4). In contrast, the mean annual fecal coliform loading from Aransas Bay to Copano Bay is 2.62×10^{13} CFU/yr. To achieve the desired mean concentration of 3.7 CFU/100ml in the bay, the mean annual watershed load must be reduced to 1.18×10^{15} CFU/yr. This represents an 85% reduction.

5.7 CONCLUSIONS FOR CHAPTER 5

In this chapter the water quality of three waterbodies in the Copano Bay watershed that are violating bacterial water quality standards and require the development of TMDLs is explored. Tidal river segments are shown to violate the water quality criteria for both the geometric mean and 75% concentration values. Bacterial water quality standards are met when modeling Copano Bay as a single waterbody (grouping all water quality data together); however, five of the seventeen sites within the bay violate the 90% value water quality standard when considering the stations individually (which is how the TCEQ regulates the bay). All sites meet the water quality standard for the median concentration. The pattern of violating Copano Bay sites points to bacterial contamination from land-based sources.

A mean annual water balance on Copano Bay reveals some interesting characteristics. Under mean annual conditions, the bay is horizontally controlled. The net interaction between Copano Bay and the atmosphere results in a loss of water from the bay. However, the amount of water flowing from Copano Bay to Aransas Bay on a net annual basis is about 5 times greater than that exiting the bay through net evaporation. A salt balance performed on the Copano-Aransas Bay system shows that the amount of water entering Copano Bay from Aransas Bay due to tidal fluctuations is approximately twice the amount that enters Copano Bay from other sources. This result gives insight to the importance of tidal interactions when considering the water quality of Copano Bay. Since the bacterial concentration in Aransas Bay is significantly lower than that in Copano Bay, tidal movement results in Aransas waters diluting the bacterial concentrations in Copano Bay. This pattern is highlighted in Figure 5.3, which shows the

TCEQ sites violating water quality standards in Copano Bay. Each of the five violating sites is located in a more secluded area of the bay away from the mixing processes between Copano and Aransas Bays.

A method is presented to use historic bacterial concentrations in the violating waterbodies to estimate the geometric mean, median, and upper percentile (75% and 90%) bacterial concentrations in the water from the output of the TMDL Balance model under (arithmetic) mean annual conditions. Assuming a constant relationship among the concentrations, the arithmetic mean bacterial concentration is reduced until the regulated concentrations meet the water quality criteria. Results are combined with flow data to compute the mean annual TMDL for each waterbody.

The TMDL Balance model described in Chapter 4 is used to model the mean annual TMDL in each of the violating waterbodies. The TMDLs are computed so that the desired mean concentration of bacteria is achieved at the SWQM sites in the waterbodies. Since watershed loading is shown to dominate the high bacterial concentrations, all other modeling parameters are held constant as the watershed load is reduced to the point that the water quality standards are met. Results of this analysis show that a 78% reduction in the bacterial load to the Mission Tidal River, a 94% reduction in the bacterial load to the Aransas Tidal River, and an 85% reduction in the bacterial load to Copano Bay are necessary.

Chapter 6: Conclusions of the Dissertation

6.1 Addressing the Research Questions

The following research questions are stated at the outset of this dissertation as the motivation for the work. Through the study presented here, we can now address these questions in the following way:

1. ***How can we combine simple modeling techniques to effectively model bacteria in the Copano Bay system?***

Two modeling approaches are used to simulate bacterial loading in the Copano Bay system. Non-tidal waterbodies are simulated with the load duration curve approach. The empirical, straightforward nature of this approach simplifies its explanation to a non-technical audience, which is particularly important when working within the TMDL program. Tidal waterbodies are modeled using the tidal prism approach, which accounts for watershed loading, tidal interactions, and first-order decay over one or more tidal cycles. Combining the tidal prism approach with a mass balance, first-order decay watershed loading model gives a straightforward approach for computing bacterial loads both throughout the watershed and in Copano Bay itself. Relationships were developed between in-stream concentrations of fecal coliform, enterococci, and *Escherichia coli* so that results of the fecal coliform loading model can be translated to other bacterial indicators. Lastly, the historic log-normal distribution of the bacterial water quality data

is used to develop a straightforward approach to using the modeled mean annual results to predict non-mean fecal coliform concentrations in the bay and tidal river segments.

2. ***How can this approach be generalized for application to a variety of pollutants and geographical locations?***

The modeling techniques were generalized through the creation of the LDCurve tool (available online for free download at http://tools.crwr.utexas.edu/LDCurve) and the TMDL Balance model. LDCurve takes advantage of CUAHSI web services and capabilities within Excel to automate the creation of fecal coliform and *E. coli* load duration curves. TMDL Balance builds upon previous successes with modeling water quality in ArcGIS to extend the use of the schematic processor to coastal systems, while accounting for tidal interactions. Basing the modeling approach on nationally available datasets increases its transferability and eases its application to watersheds outside of the immediate study area. Though the methods were developed through modeling bacterial contamination, the approach is general enough for application to a variety of pollutants.

3. ***What are the processes that affect coastal systems and create uncertainty in our modeling results and how can we quantify this uncertainty?***

Water quality sampling, statistical analyses, and uncertainty quantification shows that variations in bacterial concentrations and system hydrology cause significant uncertainty when modeling bacteria in natural systems. The load duration curve approach accounts for a portion of this uncertainty by presenting bacterial loading under

the full hydrologic regime. Implications of uncertainty were not completely quantified using the TMDL Balance model due to a lack of information. However, a First Order Analysis of Uncertainty was used to quantify the impact of uncertainty in select parameters on the variance in modeling results. This analysis verifies the difficulty of accurately modeling bacteria in natural systems, resulting in a coefficient of variation of greater than one.

6.2 CONTRIBUTIONS TO SCIENCE AND TECHNOLOGY

Contributions of this research include

1) The creation of modeling tools to directly address the needs put forth by the Bacteria TMDL Task Force.
2) The development of an automated, reproducible method to create load duration curves in a matter of minutes instead of hours.
3) A proof-of-concept in using CUAHSI web services for modeling water quality in non-tidal waterbodies.
4) A proof-of-positive-correlation between hydrologic conditions and bacterial concentrations in the Copano Bay watershed.
5) Insight to the limited role that wastewater treatment plants play in bacterial contamination in the Copano Bay watershed.
6) The development of a linear relationship between log-transformed in-stream concentrations of fecal coliform, *E. coli*, and enterococci in the study area.
7) The extension of use of the schematic processor to tidal waterbodies through the inclusion of the tidal prism approach.

8) A water quality modeling approach that is based around a nationally available dataset, generalizing its application to watersheds across the nation.
9) An initial quantification of the uncertainty involved with modeling bacterial loads in coastal watersheds.
10) A quantification of the mean annual water and pollutant balance in the Copano Bay system.
11) Insight into the importance of tidal interactions in the water quality of Copano Bay.
12) An approach for using mean annual concentrations of fecal coliform in the Mission and Aransas Tidal Rivers and Copano Bay to predict other probabilistic concentrations in these waterbodies.

6.3 RECOMMENDATIONS FOR FUTURE WORK

The following recommendations are made for future work to improve upon the research presented here:

1) Extend the use of the LDCurve tool.

   The LDCurve tool is currently designed to access water quality data only within the State of Texas. Updating the tool to access water quality on a national scale would make it more valuable to practitioners. Also, results from the tool would be more accurate if LDCurve modeled individual SWQM stations instead of segments and included methods to more accurately estimate the mean daily flow at the modeled location. Reprogramming the code to use a STORET web service (once developed) would enable the tool's use nationwide and negate the concern of spatial discrepancies between flow and water quality data. Extending LDCurve to use personal datasets and including methods for translating flows between sites (such as the Drainage-Area Ratio Method) also would be beneficial.

2) Further quantify the spatial and temporal variation in bacterial loading in the Copano Bay watershed.

   Water quality monitoring in the Copano Bay watershed should continue toward the goal of continuously monitored bacterial concentrations at select locations within the watershed. Continuous data would give further insight into the cause and effect relationships around bacterial concentrations. Continuous streamflow data also should be collected at these sites to allow translation of concentrations to loads.

3) Include internal loading in the TMDL Balance model.

   Other studies have shown that bacterial sources internal to waterbodies (such as regrowth and resuspension) can contribute significantly to overall bacterial loading. Lack of data in the Copano Bay watershed disallowed the inclusion of these potential sources in the TMDL Balance model. However, results of the model calibration indicate that internal bacteria sources may be present. Work should be done to characterize bacterial sources internal to the bay and tidal rivers and, once characterized, TMDL Balance modeling equations should be updated to include these terms.

4) Characterize the tidal exchange between the tidal river sections and Copano Bay.

   More data are needed to characterize the tidal interactions between the tidal river segments and Copano Bay. These data may be in the form of salinity measurements or readings from flow meters. Once this interaction is better understood, the tidal prism method should be applied to the tidal river segments, accounting for loading to the rivers from Copano Bay.

5) Characterize the impact of failing on-site sewage facilities around the bay.

   Given their proximity, the potential for failing on-site sewage facilities (OSSFs) in the communities immediately surrounding the bay to contribute significant loads of bacteria to the bay is notable. Soils in the area around the bay are considered inappropriate for conventional septic systems, due in part to high water tables, but a large portion of the homes in the area are using this method of waste disposal. Results of the TMDL Balance model show that under mean annual conditions, human sewage accounts for a significant fecal coliform loading into the bay. However, the assumptions made to estimate the number of and

loadings from failing septic systems are based on limited data and have the potential for large uncertainty. A better understanding of actual failure rates and movement of the sewage is necessary to accurately quantify the impact of this source and design approaches to alleviate the problem.

Appendix A: Generating a Schematic Network from NHDPlus Features

Generating a Schematic Network from NHDPlus Data

Ernest To and Stephanie L. Johnson

Necessary Software and Assumptions

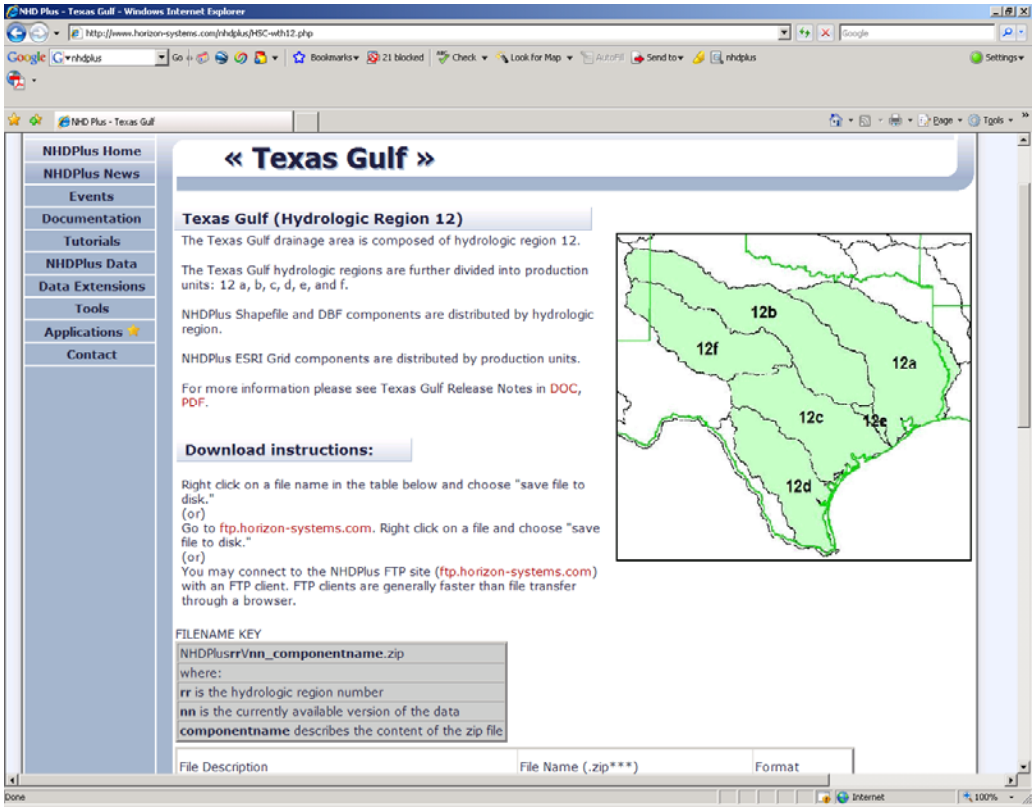
This exercise was written using ArcMap version 9.2, Arc Hydro Tools version 1.3, the Network Analyst Tools, the Utility Network Analyst Tools, and the Visual Basic Editor. The text is intended for a user with a working knowledge of (and access to) these software and tools. (The most recent version of the Arc Hydro Tools can be downloaded from the ESRI Arc Hydro Online data support system at: http://support.esri.com/index.cfm?fa=downloads.dataModels.filteredGateway&dmid=15. You will need to install both the ApFramework and Arc Hydro setup files.) Upon completing this exercise, the user will have learned to download NHDPlus data, modify NHDPlus data for use with the Arc Hydro "Node/Link Schema Generation" tool, create a schematic network for a watershed, and connect a schematic network to a bay for modeling purposes.

Part I: Extracting hydrological features from NHDPlus for a waterbody

Phase I: Download NHDPlus

1. Open up your web browser and navigate to the NHDPlus website: http://www.horizon-systems.com/nhdplus. Click on ***NHDPlus Data*** in the left menu. You will encounter a map of the United States. This map allows you to

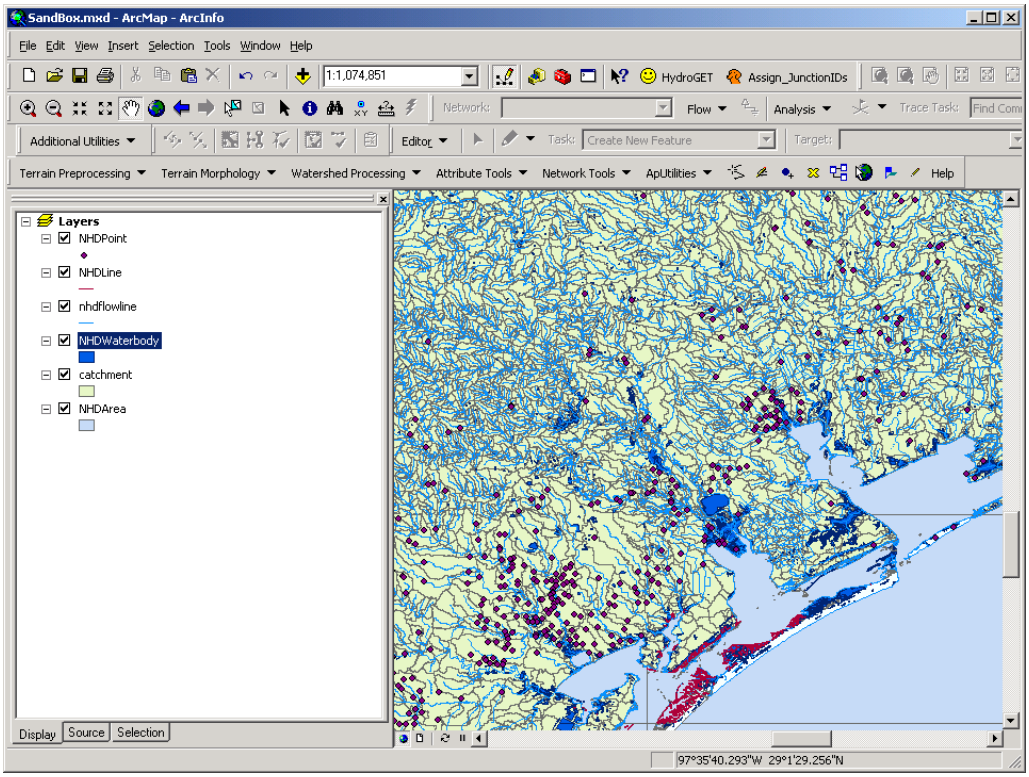
zoom into a U.S. region where you can download its associated NHD data. For this exercise, we will select the Texas Gulf region. Clicking on the region in the map brings you to the following webpage:



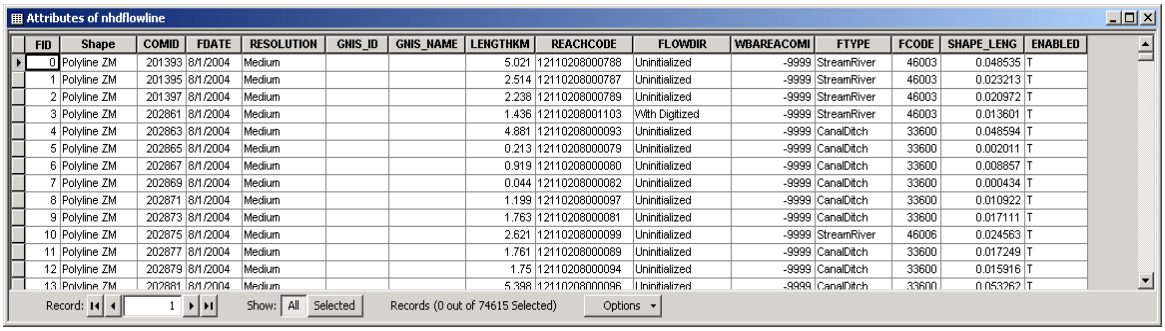
To build a schematic network, you only need the catchment and NHD shapefiles. The connectivity and flow direction are already established within the NHD flowlines. You can download the quality assurance/quality control (QA/QC) sinks in case you want to check for anomalies.

File Description	File Name (.zip***)	Format
Region 12, Version 01_02, Catchment Shapefile	***NHDPlus12V01_02_Catshape***	***Shapefile****
Region 12, Version 01_01, National Hydrography Dataset	***NHDPlus12V01_02_NHD***	***Shapefile and DBF***
Region 12, Version 01_01, QAQC & Sinks Spreadsheet	***NHDPlus12V01_01_QAQC_Sinks***	***Excel Spreadsheet***

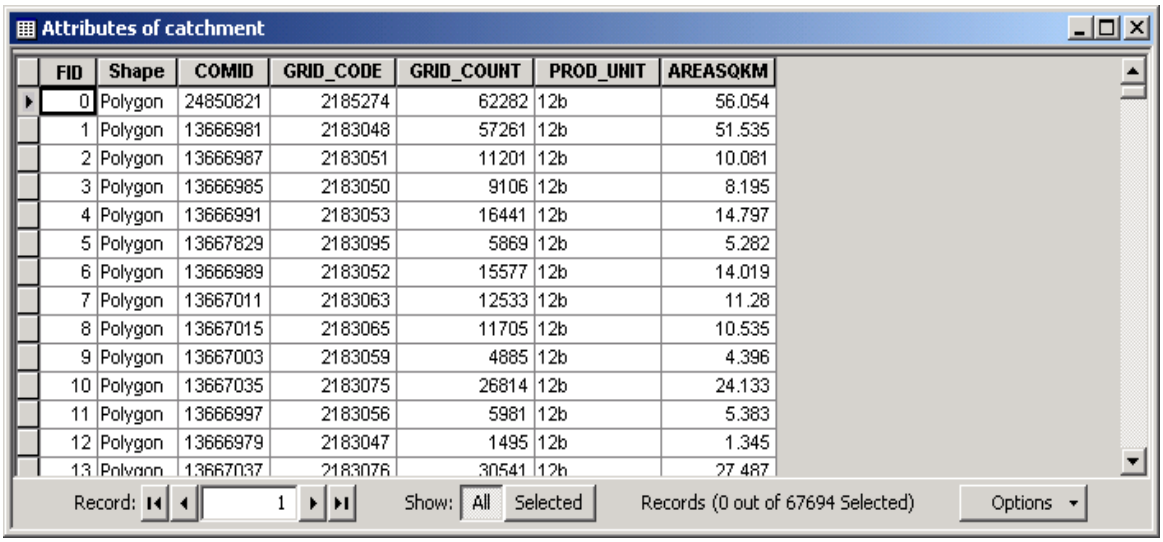
2. Unzip the download zip files and bring the shapefiles into ArcMap. The figure below shows the downloaded catchments and hydrography along the Texas coast.



3. Open up the attribute table of NHDFlowline and take a look at it.



4. Open up the attribute table of NHDPoint and take a look at it.

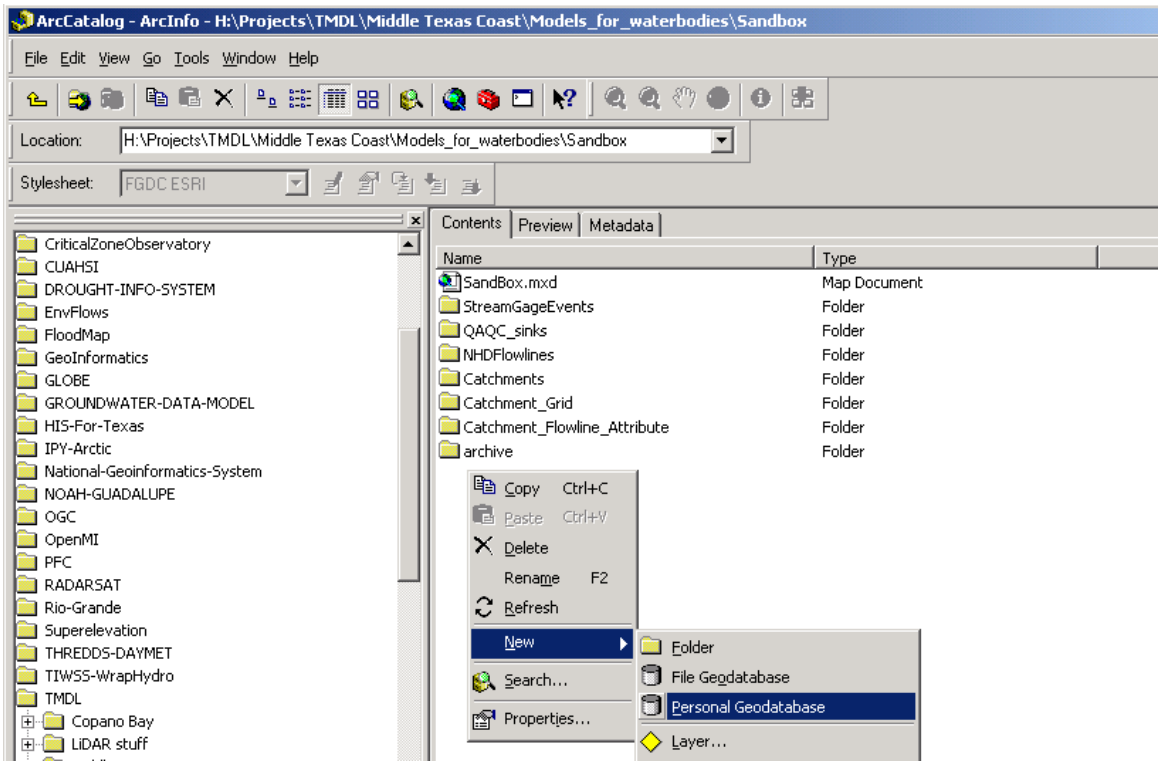


Congratulations, you have downloaded NHDPlus data from the internet.

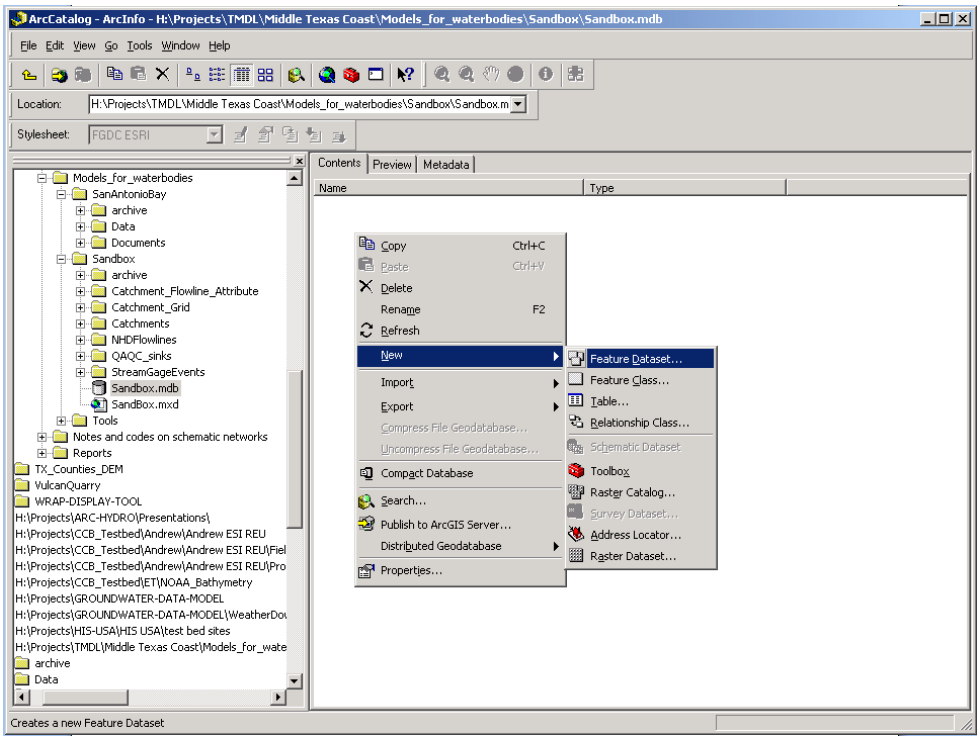
Phase II: Ingest NHDPlus into a geodatabase

In this phase we will create a geodatabase and load the NHDPlus data into it. This is necessary because we will create a geometric network of the hydrography and can only do so only within a geodatabase.

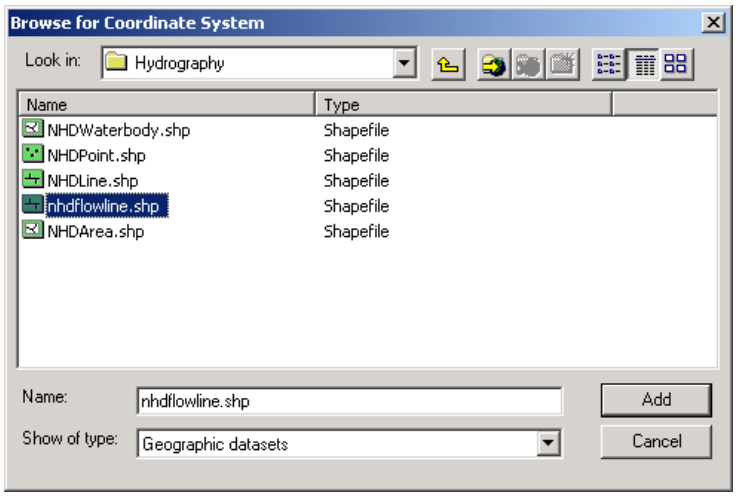
1. Open up ArcCatalog and navigate to a folder where you want to place your geodatabase. Create an empty geodatabase in the folder by right clicking within the empty space in the ***Contents*** window, select ***New*** and ***Personal Geodatabase***.



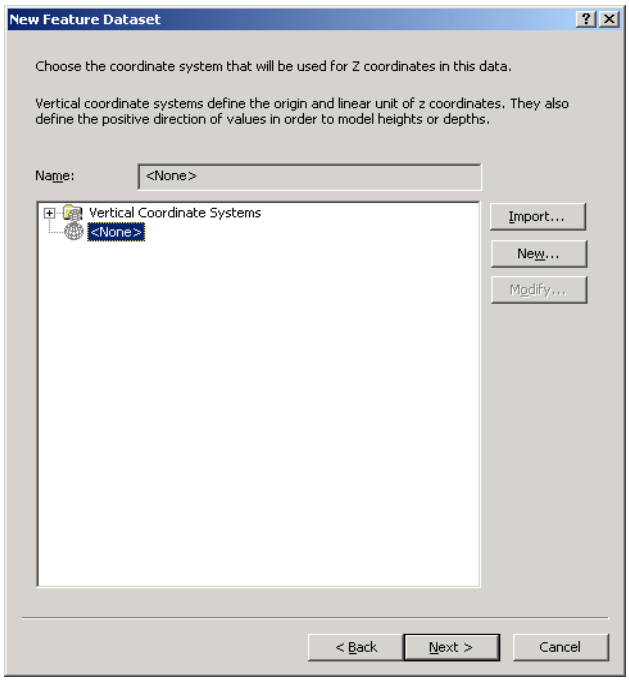
2. Open the geodatabase and create a new Feature Dataset called “Hydrography” in the geodatabase.



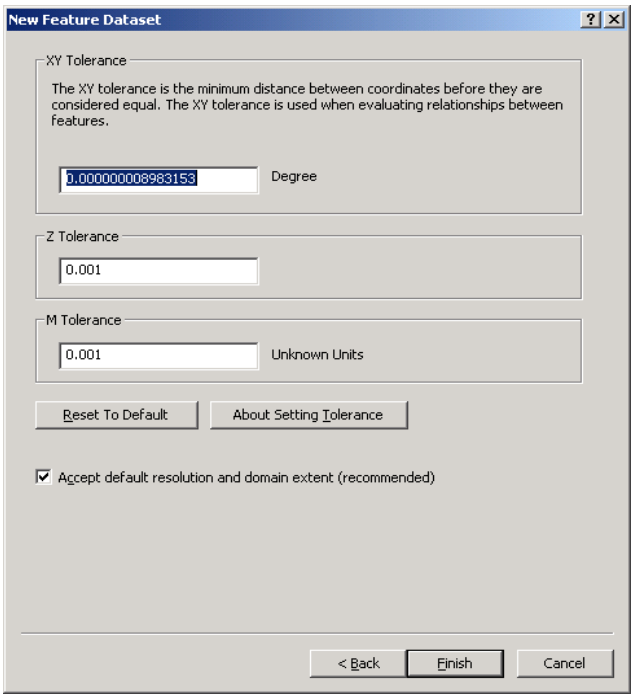
3. Give this data set the same coordinate system as NHDFlowline, which is NAD1983.



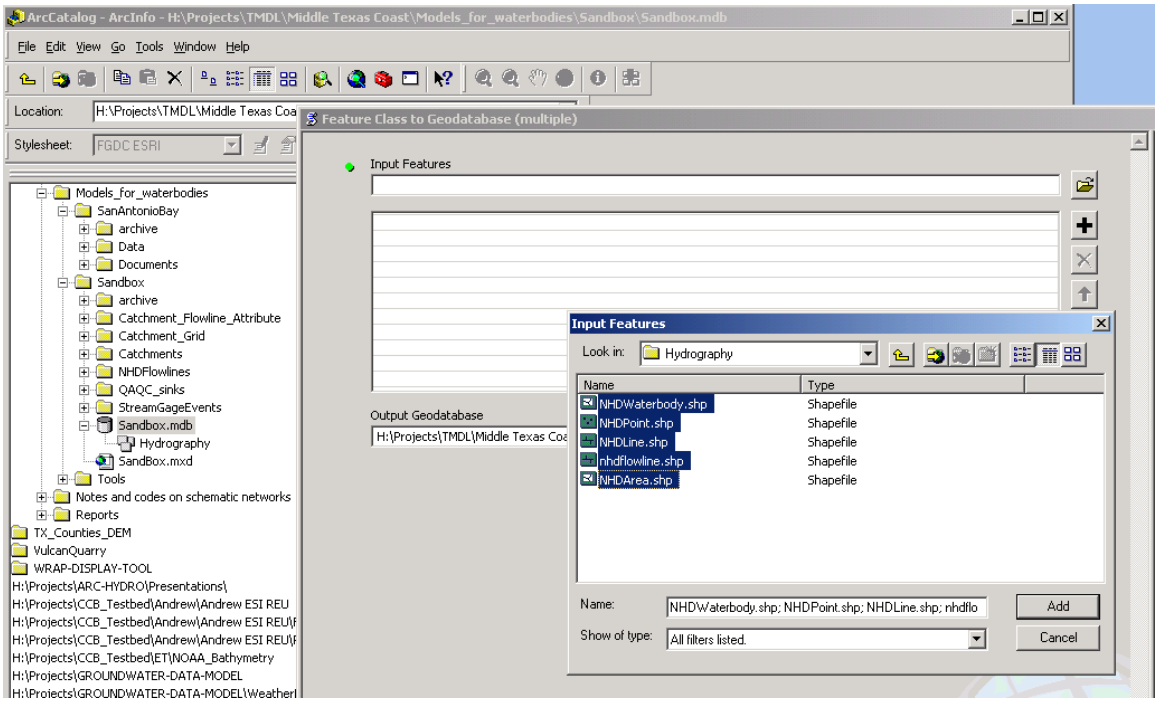
4. Skip the vertical coordinate system. We will not use vertical data in this exercise.



5. Keep the default tolerances.



6. Import featureclasses relevant to schematic network generation into the ***Hydrography*** dataset (takes about 15 minutes). These are NHDWaterbody, NHDPoint, NHDLine, NHDflowline and NHDArea. Simply right click on the geodatabase icon and select ***Feature Class to Geodatabase (multiple)***.


ArcCatalog - ArcInfo - H:\Projects\TMDL\Middle Texas Coast\Models_for_waterbodies\Sandbox\Sandbox.mdb
File Edit View Go Tools Window Help
Location: H:\Projects\TMDL\Middle Texas Coa
Stylesheet: FGDC ESRI
Models_for_waterbodies
SanAntonioBay
archive
Data
Documents
Sandbox
archive
Catchment_Flowline_Attribute
Catchment_Grid
Catchments
NHDFlowlines
QAQC_sinks
StreamGageEvents
Sandbox.mdb
Hydrography
SandBox.mxd
Tools
Notes and codes on schematic networks
Reports
TX_Counties_DEM
VulcanQuarry
WRAP-DISPLAY-TOOL
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Input Features
Output Geodatabase
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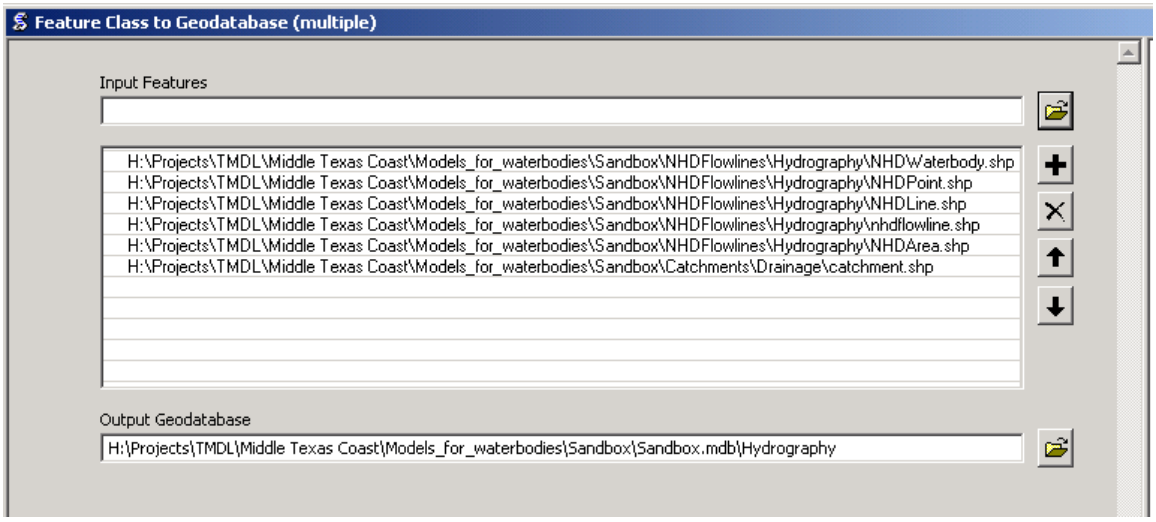
Input Features
Look in: Hydrography
Name
Type
NHDWaterbody.shp
Shapefile
NHDPoint.shp
Shapefile
NHDLine.shp
Shapefile
nhdflowline.shp
Shapefile
NHDArea.shp
Shapefile
Name: NHDWaterbody.shp; NHDPoint.shp; NHDLine.shp; nhdflo
Add
Show of type: All filters listed.
Cancel


Feature Class to Geodatabase (multiple)
Input Features
H:\Projects\TMDL\Middle Texas Coast\Models_for_waterbodies\Sandbox\NHDFlowlines\Hydrography\NHDWaterbody.shp
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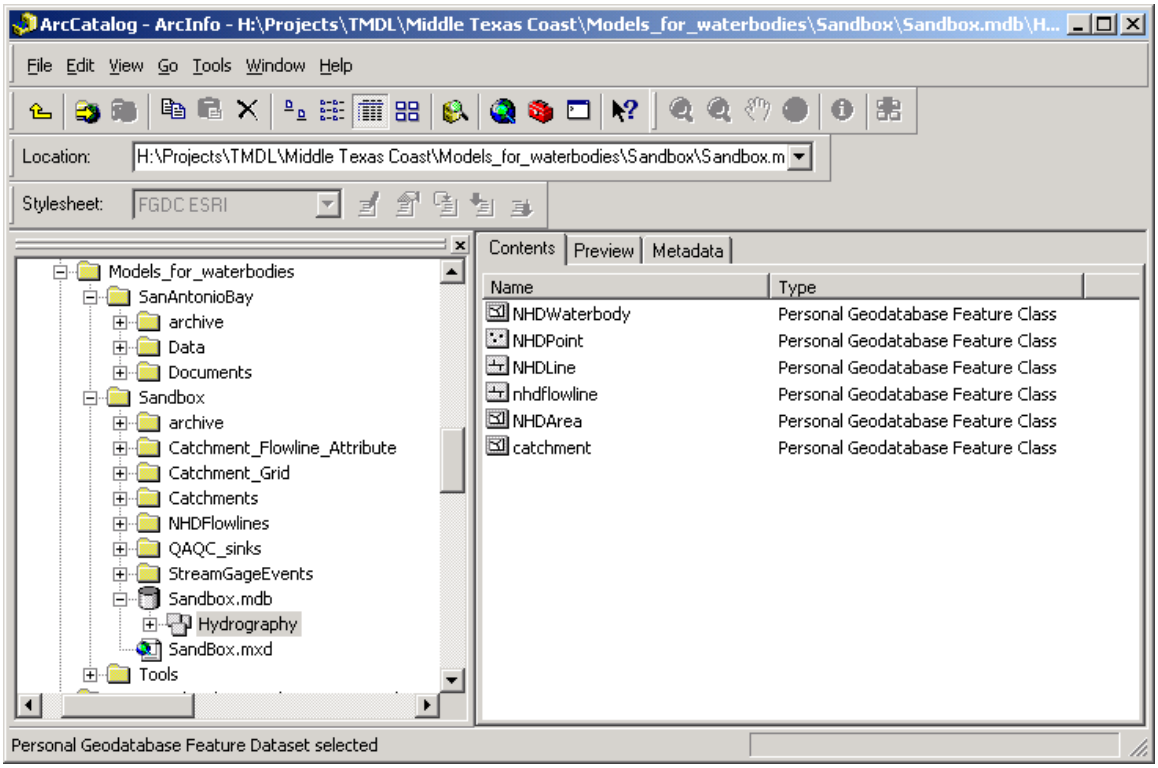
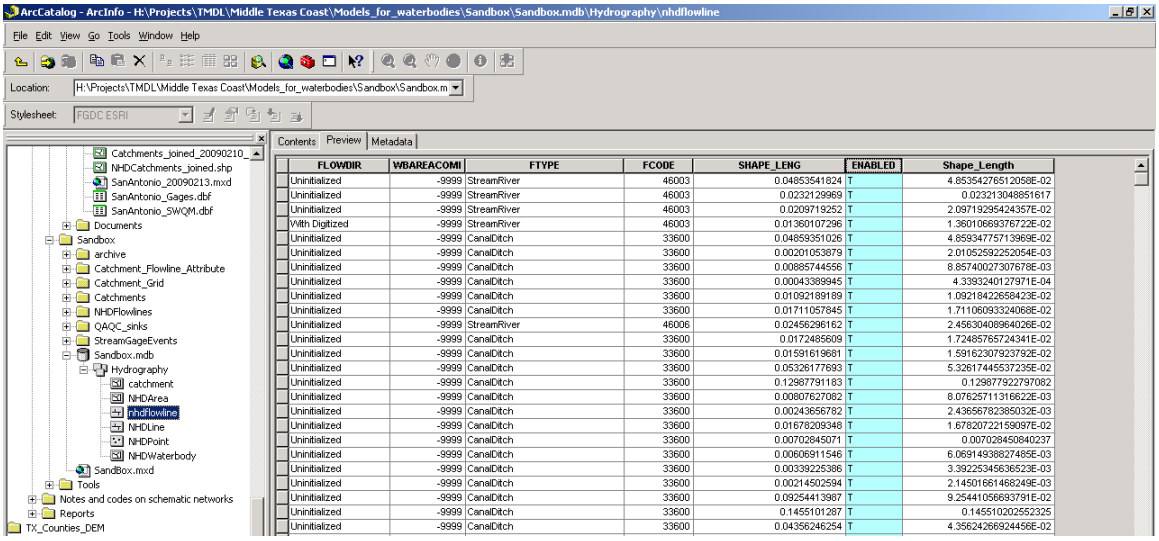
H:\Projects\TMDL\Middle Texas Coast\Models_for_waterbodies\Sandbox\Catchments\Drainage\catchment.shp
Output Geodatabase
H:\Projects\TMDL\Middle Texas Coast\Models_for_waterbodies\Sandbox\Sandbox.mdb\Hydrography



Phase III: Build a geometric network

Using the NHDPlus data, we will create a geometric network that describes the flow and connectivity of the NHDflowlines. Using this network we can trace the contributing area to specific water bodies within the Texas Gulf Region.

1. Before we start, we need to first make sure the NHD data are properly formatted before building a geometric network.
2. Open up the attribute table of NHDFlowline. Note that the ***Enabled*** field in the attribute table is a string field instead of a Boolean field. This will interfere with the creation of a network. Delete this field.



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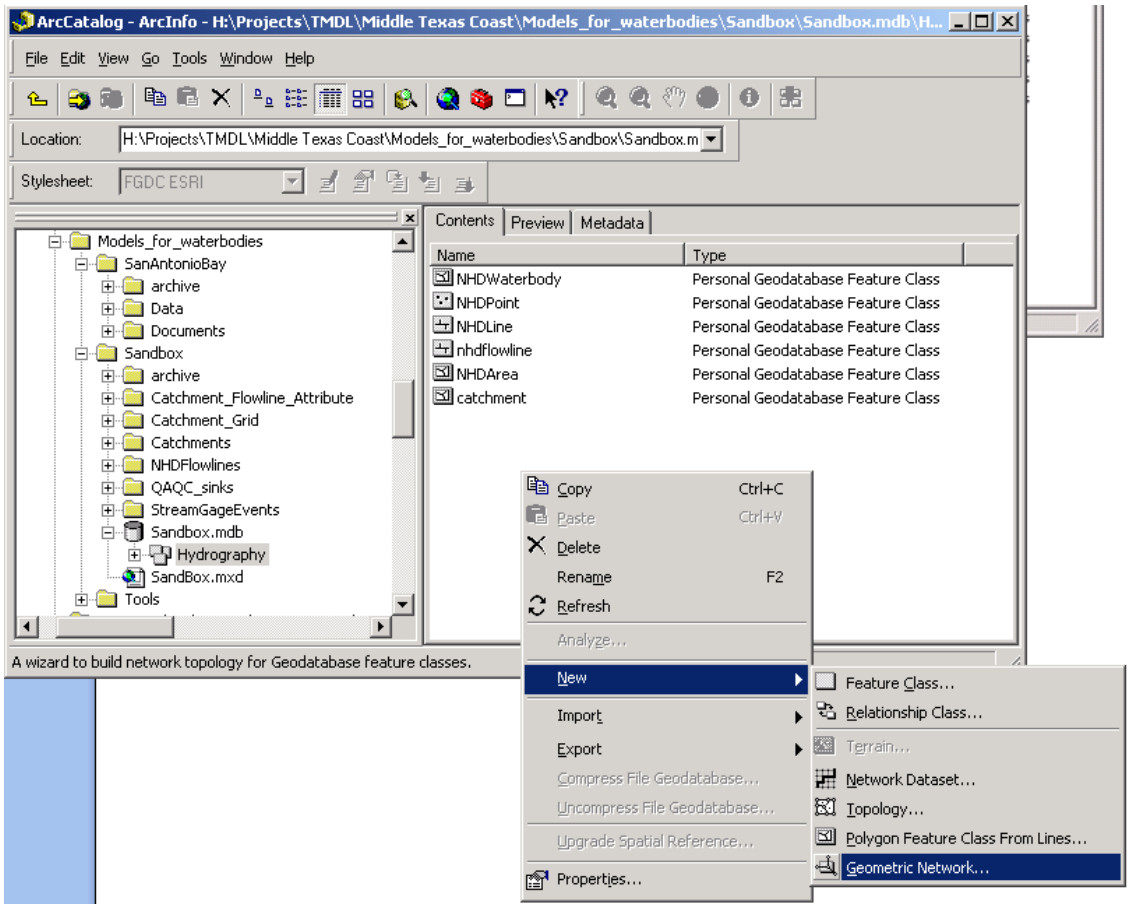
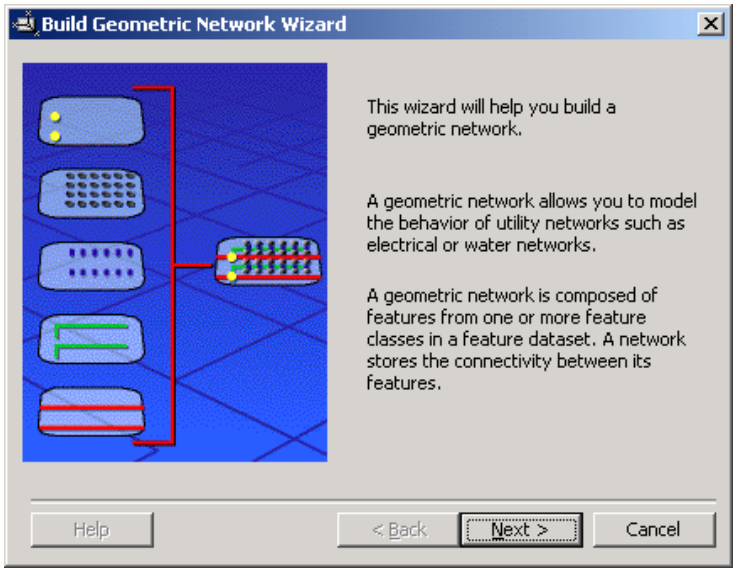
Uninitialized	-9999	StreamRiver	46003	0.0232129969	T	0.023213048851617
Uninitialized	-9999	StreamRiver	46003	0.0209719252	T	2.09719295424357E-02
With Digitized	-9999	StreamRiver	46003	0.01360107296	T	1.36010669376722E-02
Uninitialized	-9999	CanalDitch	33600	0.04859351026	T	4.85934775713969E-02
Uninitialized	-9999	CanalDitch	33600	0.00201053879	T	2.01052592252054E-03
Uninitialized	-9999	CanalDitch	33600	0.00885744556	T	8.85740027307678E-03
Uninitialized	-9999	CanalDitch	33600	0.00043389945	T	4.3393240127971E-04
Uninitialized	-9999	CanalDitch	33600	0.01092189189	T	1.09218422658423E-02
Uninitialized	-9999	CanalDitch	33600	0.01711057845	T	1.71106093324068E-02
Uninitialized	-9999	StreamRiver	46006	0.02456296162	T	2.45630408964026E-02
Uninitialized	-9999	CanalDitch	33600	0.0172485609	T	1.72485765724341E-02
Uninitialized	-9999	CanalDitch	33600	0.01591619681	T	1.59162307923792E-02
Uninitialized	-9999	CanalDitch	33600	0.05326177693	T	5.32617445537235E-02
Uninitialized	-9999	CanalDitch	33600	0.12987791183	T	0.129877922797082
Uninitialized	-9999	CanalDitch	33600	0.00807627082	T	8.07625711316622E-03
Uninitialized	-9999	CanalDitch	33600	0.00243656782	T	2.43656782385032E-03
Uninitialized	-9999	CanalDitch	33600	0.01678209348	T	1.67820722159097E-02
Uninitialized	-9999	CanalDitch	33600	0.00702845071	T	0.007028450840237
Uninitialized	-9999	CanalDitch	33600	0.00606911546	T	6.06914938827485E-03
Uninitialized	-9999	CanalDitch	33600	0.00339225386	T	3.39225345636523E-03
Uninitialized	-9999	CanalDitch	33600	0.00214502594	T	2.14501661468249E-03
Uninitialized	-9999	CanalDitch	33600	0.09254413987	T	9.25441056693791E-02
Uninitialized	-9999	CanalDitch	33600	0.1455101287	T	0.145510202552325
Uninitialized	-9999	CanalDitch	33600	0.04356246254	T	4.35624266924456E-02

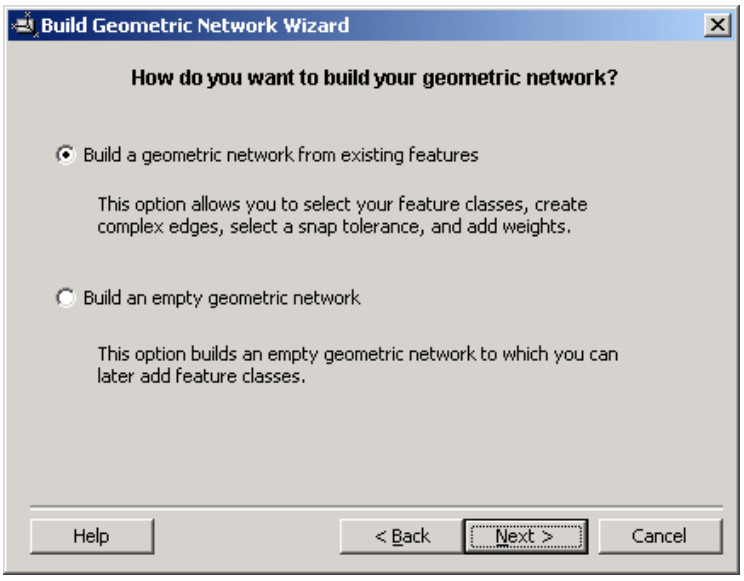
3. Within the ***Hydrography*** dataset, create a new geometric network by right clicking within the ***Contents*** window, select ***New*** and ***Geometric Network***.



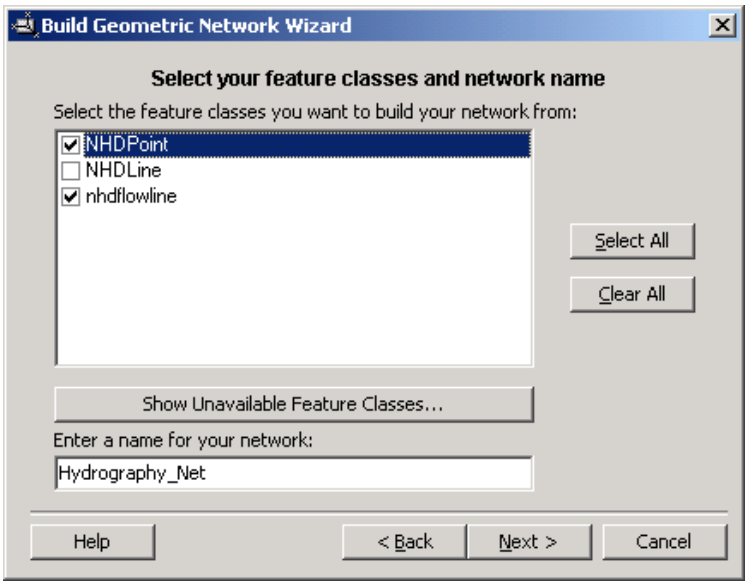
4. In the following window, choose ***Next***.



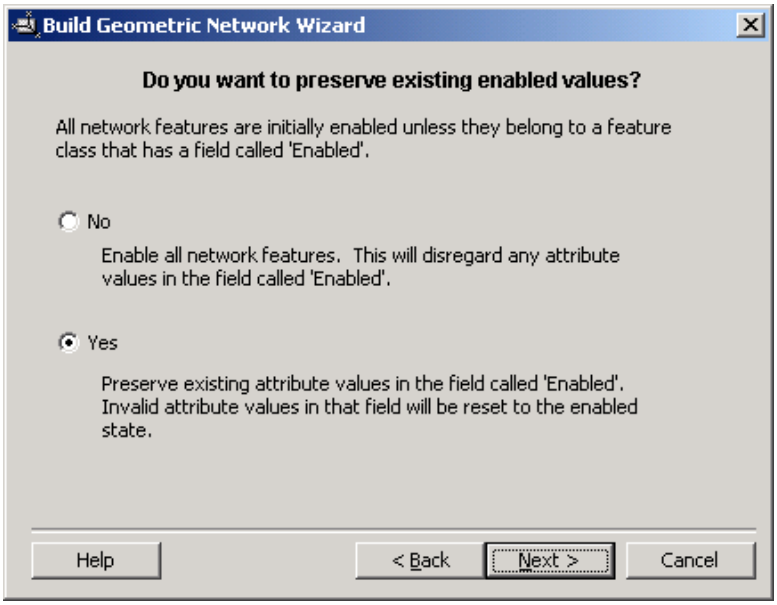
5. Again, in the next window, choose ***Next***.



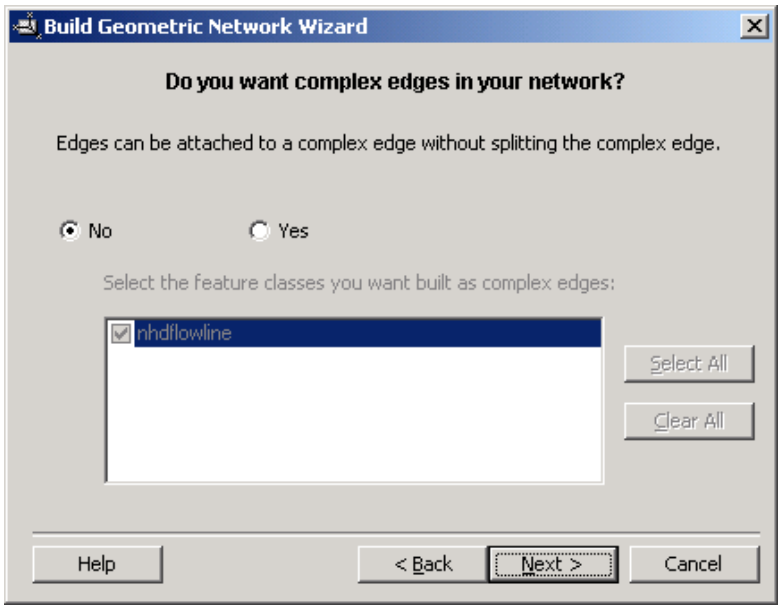
6. Now we select NHDPoint and NHDFlowline as the inputs to the network.



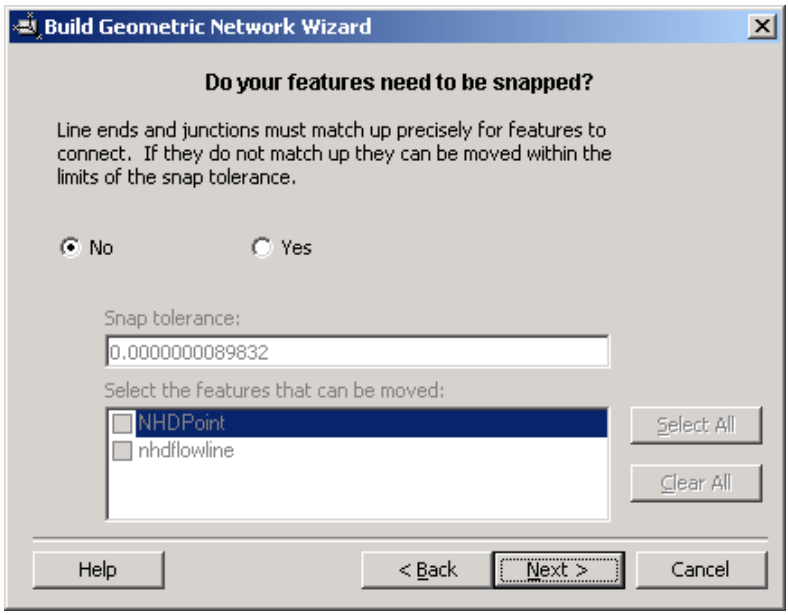
7. In the following window, choose ***Next***.



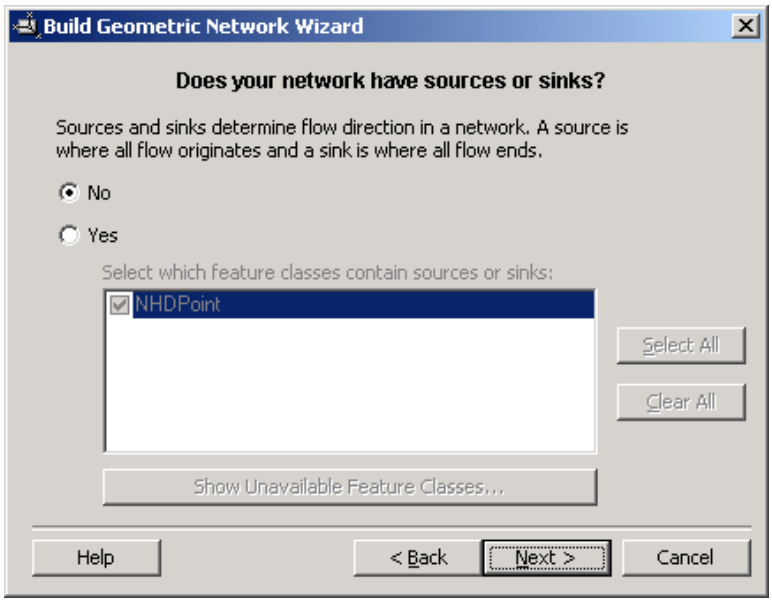
8. In the following window, choose ***Next***.



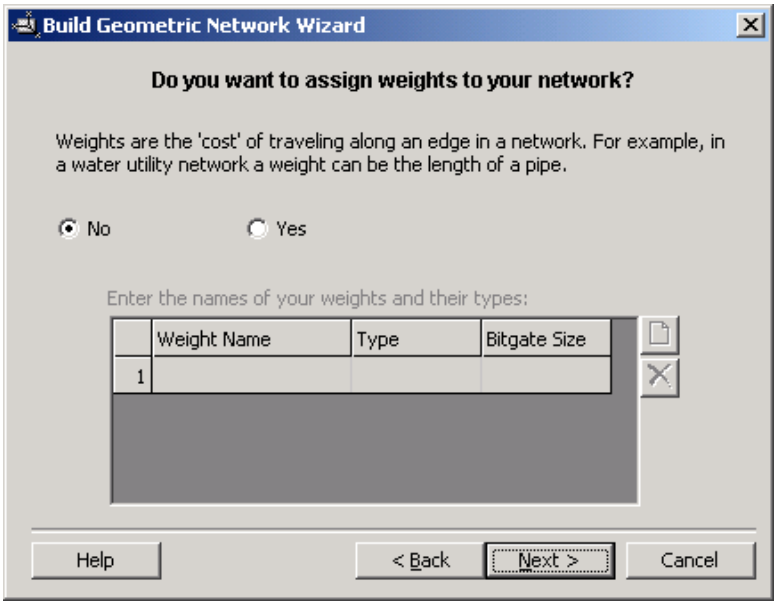
9. Again, choose ***Next***.



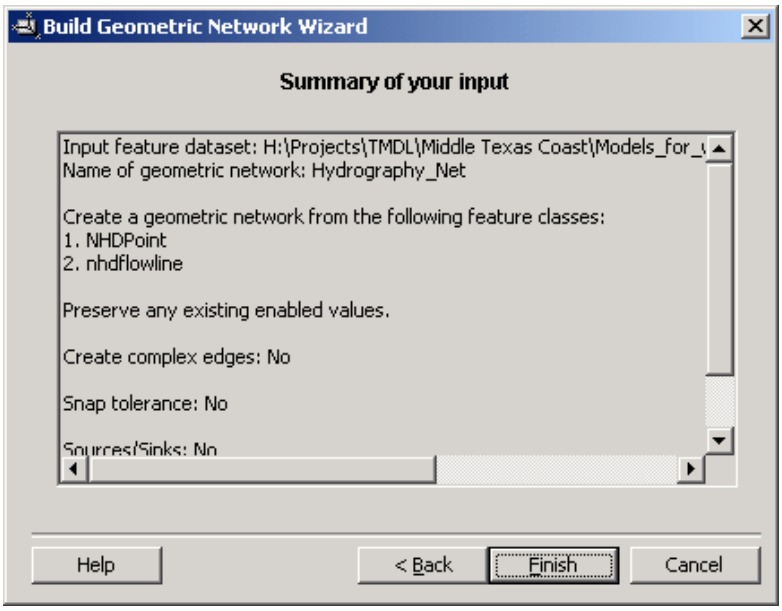
10. In the following window, choose ***Next***.



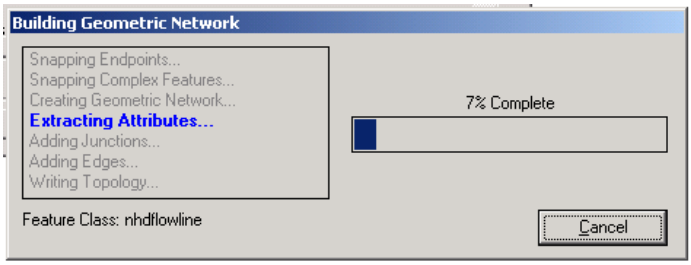
11. In the following window, choose ***Next***.



12. In the following window, choose ***Next***.

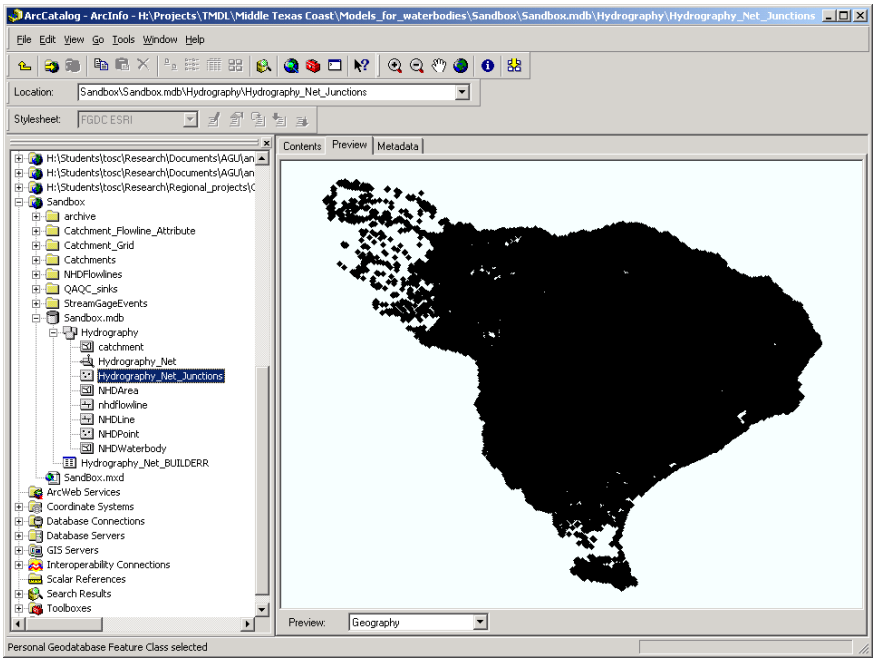


13. In the following window, choose ***Next***. The network will now be built. This process could take a while to complete. Be patient and wait for it to complete its work.

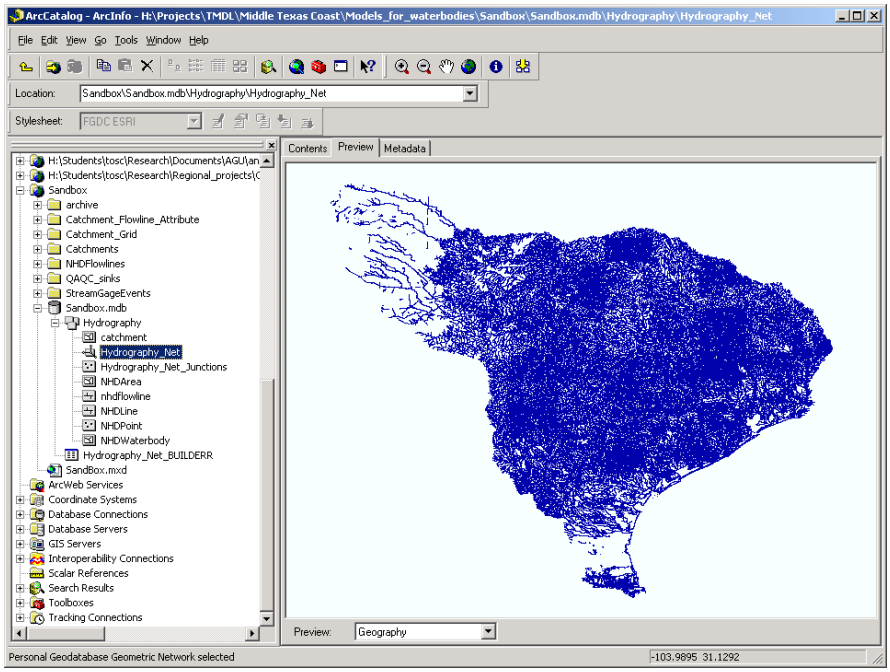


14. ArcCatalog may hang after finishing building the network. If that happens, simply close the application using Windows Task Manager and restart

ArcCatalog. The diagram below shows the junctions of the Geometric Network that was created for the Texas Gulf Region.

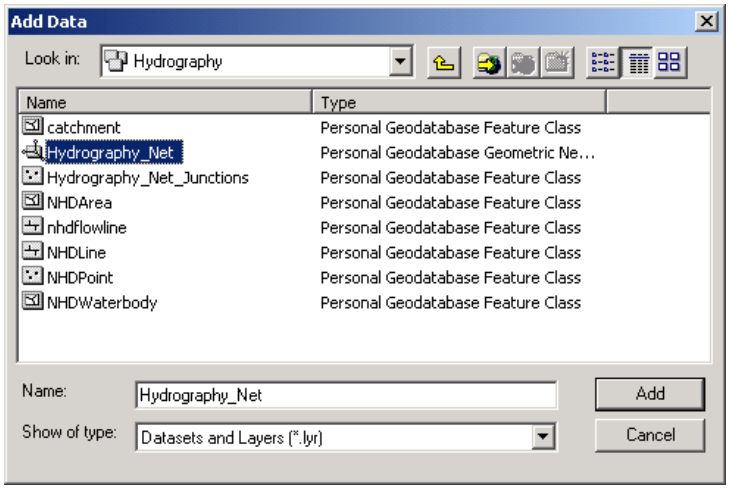


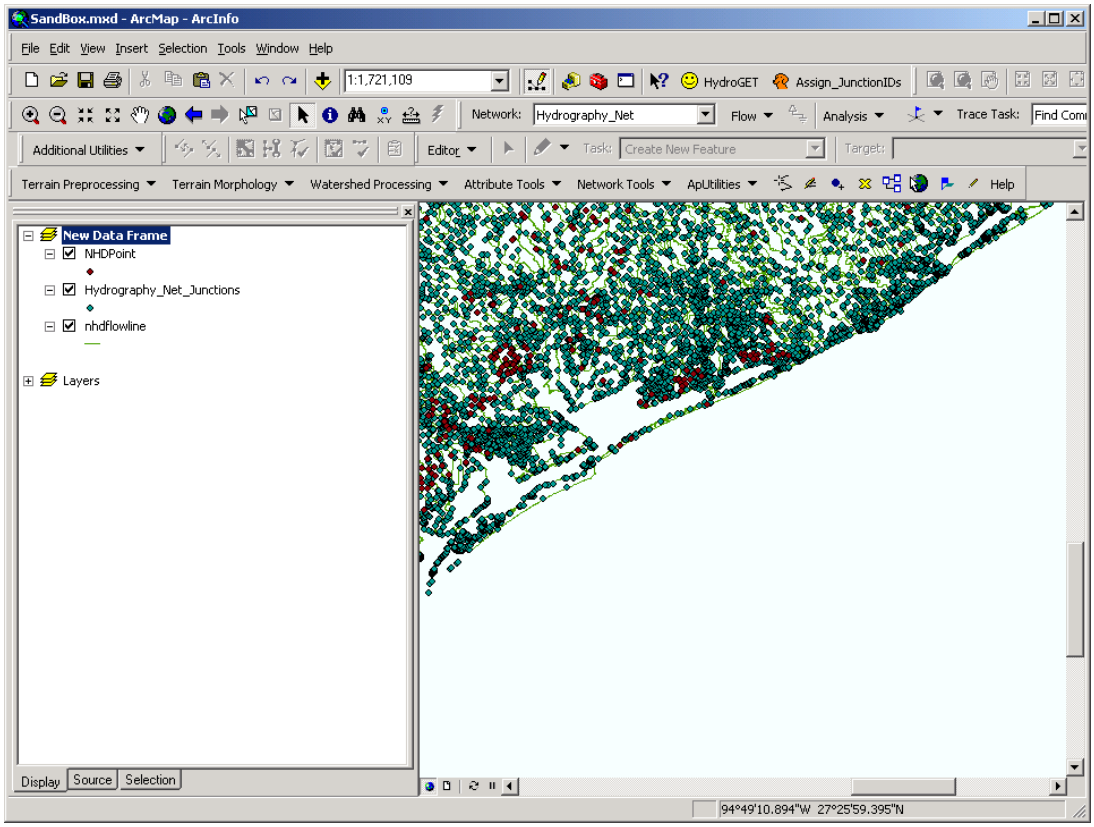
The diagram below shows the flowlines of the Geometric Network of the Texas Gulf Region.



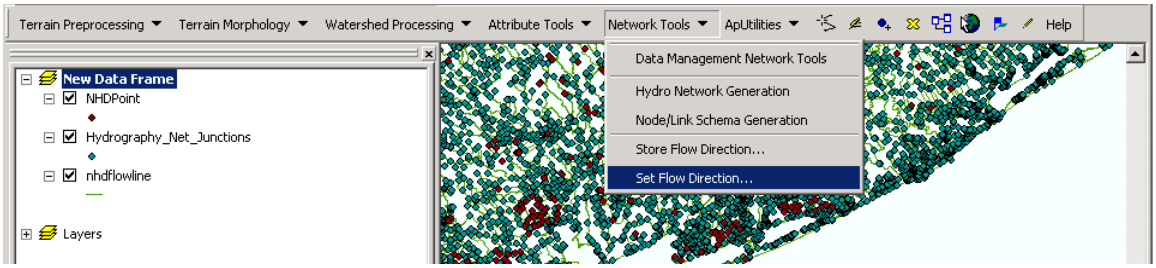
Phase IV: Set flow direction for a geometric network

1. Open up ArcMap and bring in the geometric network that you just created.

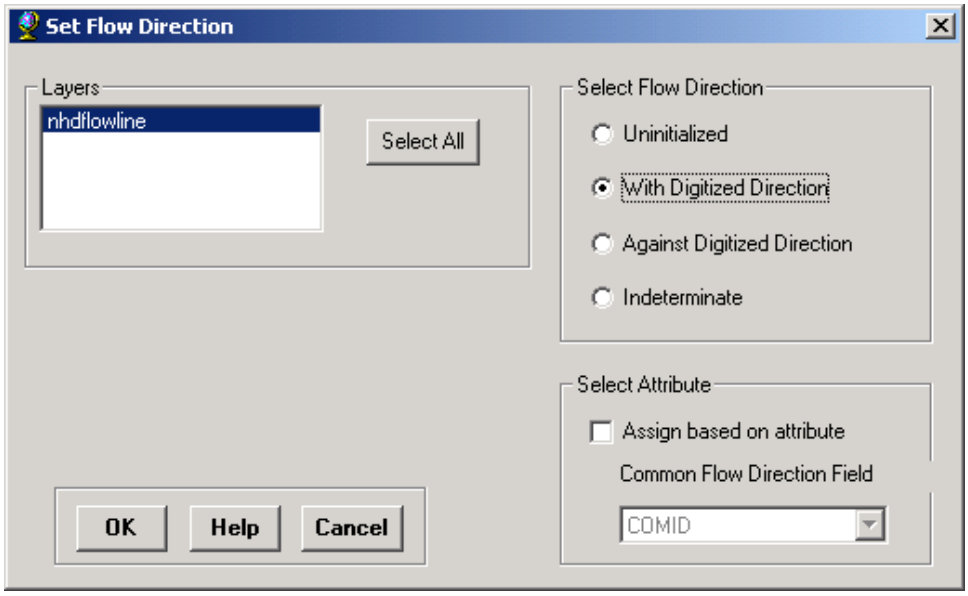




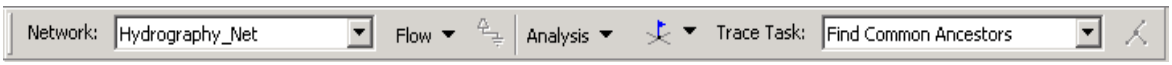
2. Make sure you have the Arc Hydro Toolbar viewable. (You can make it viewable by selecting ***View/Toolbars/Arc Hydro Tools 9***. If this toolbar is not an option, see the beginning of the tutorial for detailing on downloading the Arc Hydro Tools.) Then go to the ***Arc Hydro*** toolbar, navigate to ***Network Tools*** and click on ***Set Flow Direction***.



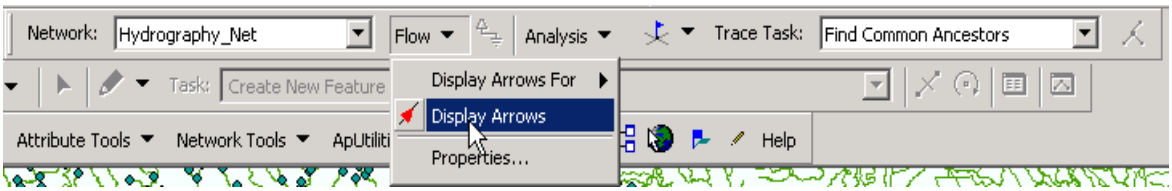
3. Specify that you are selecting flow direction ***with digitized direction***. This may take a while to process.



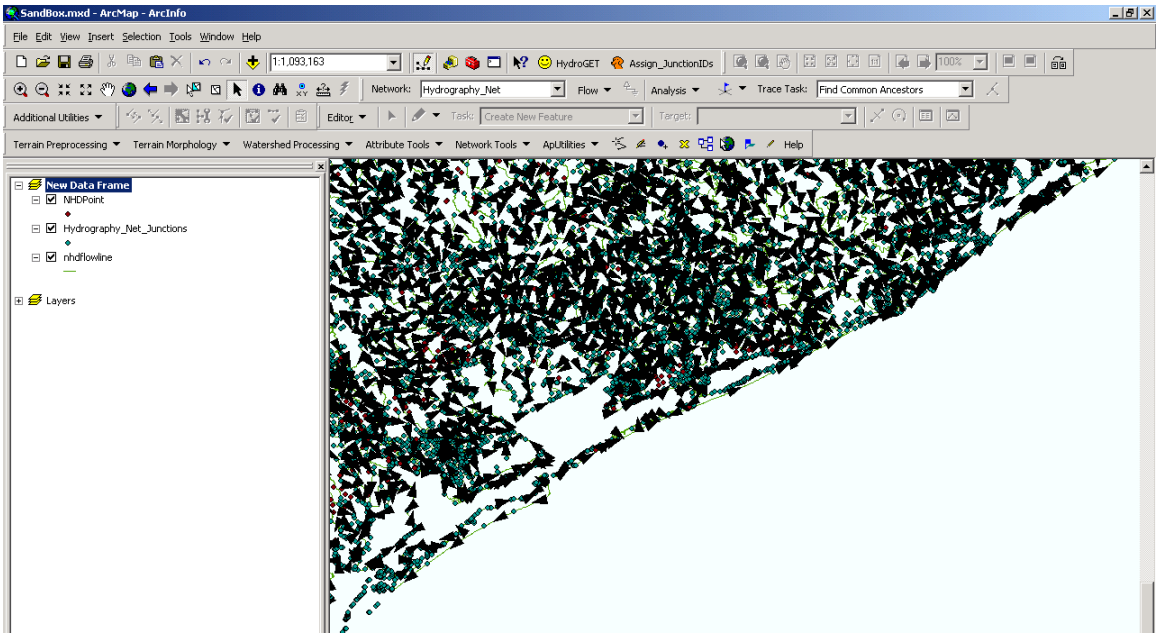
4. Next make sure you have the Utility Network Analyst toolbar enabled.



5. Check the flow direction for the geometric network by navigating to ***Flow*** and then ***Display Arrows.***



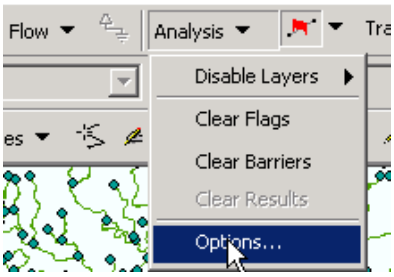
6. The flow direction arrows will show up on the map.



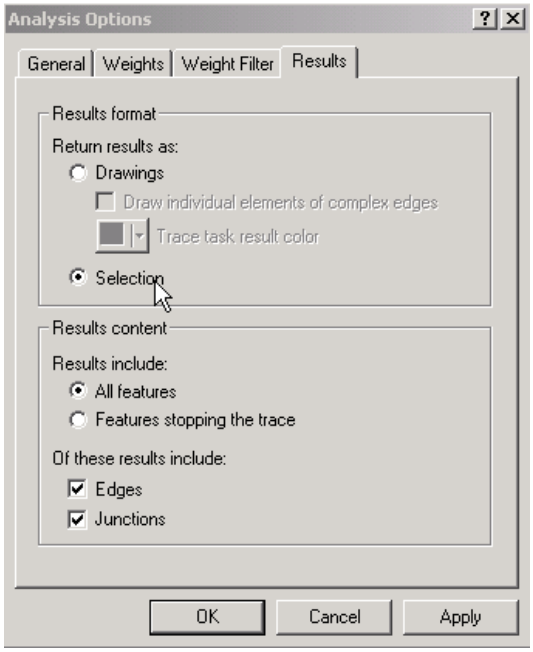
Phase V: Identify the watershed of a bay by tracing upstream

OK, let's pick one of the bays and trace upstream from its coastline. For this example, we'll use San Antonio Bay. Tracing upstream selects the flowlines, junctions, and points that contribute to San Antonio Bay. Essentially, this allows us to see the geometric network features that are part of the San Antonio watershed.

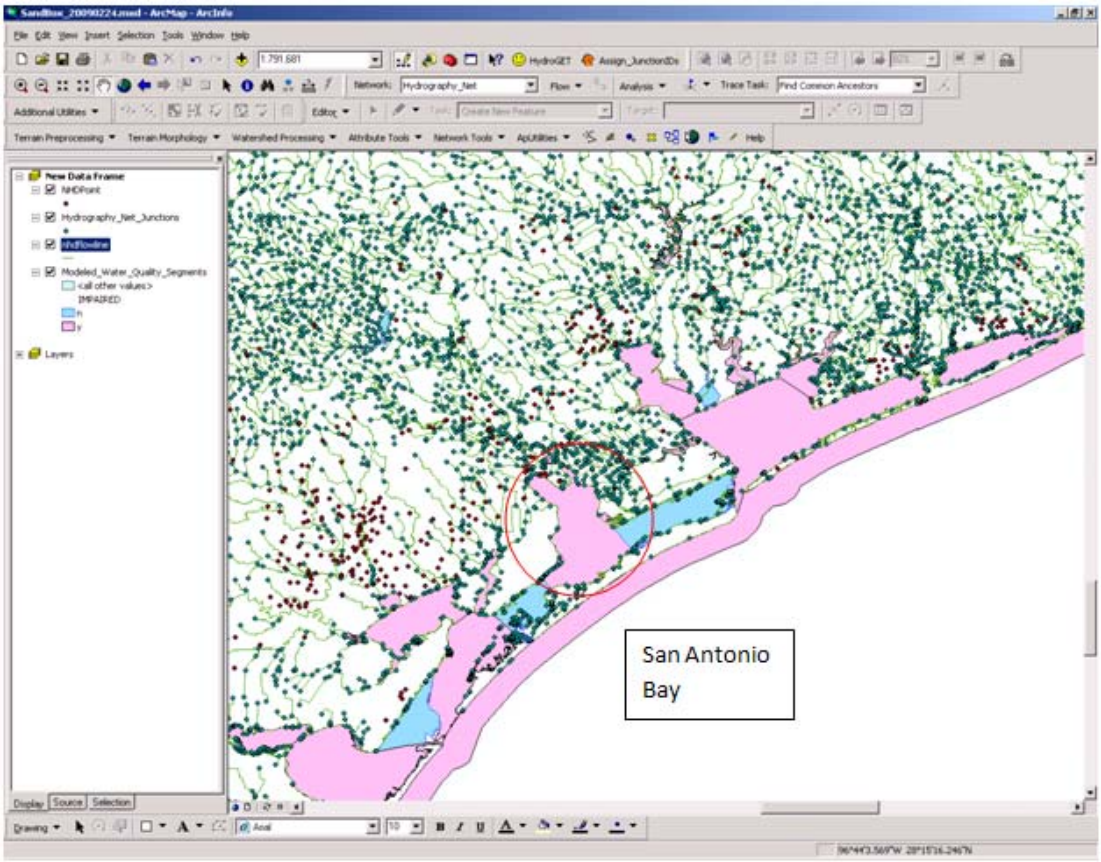
1. Before we start, let's set the options for tracing so that results are returned as a selection. In the ***Network Analyst*** toolbar, click on ***Analysis*** then select ***Options***.



2. Select ***Return results as Selection***. Hit OK.



3. Now we bring in a shapefile of the Texas bays so that we can find the location of San Antonio Bay.

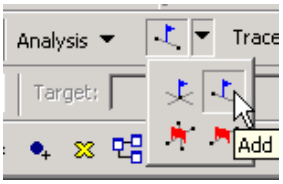


4. We will trace San Antonio Bay by placing two flags along its coastline:

   i) one flag at the eastern edge of the San Antonio coastline. This will serve as the source of the trace.

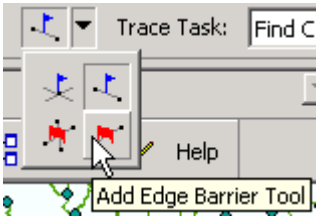
   ii) one flag at the western edge of the San Antonio coastline. This will serve as a barrier to the trace. Note: NHDPlus treats the Texas coastline like a stream that flows eastwards along the gulf. Without the barrier flag, the upstream tracing will include watersheds of the bays west of San Antonio Bay.

5. In the network analysis toolbar, click on the **add edge flag tool** button and then click on the eastern edge of the shoreline.

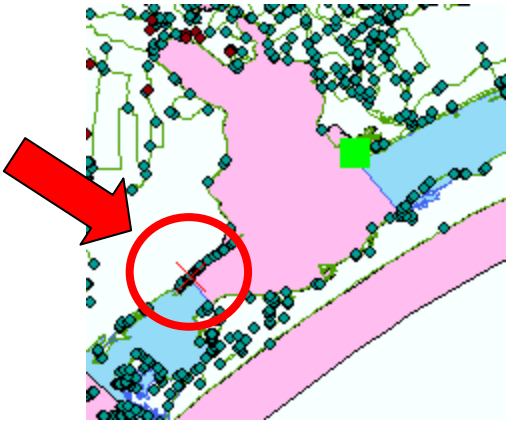


The position of the flag will be marked with a green box.

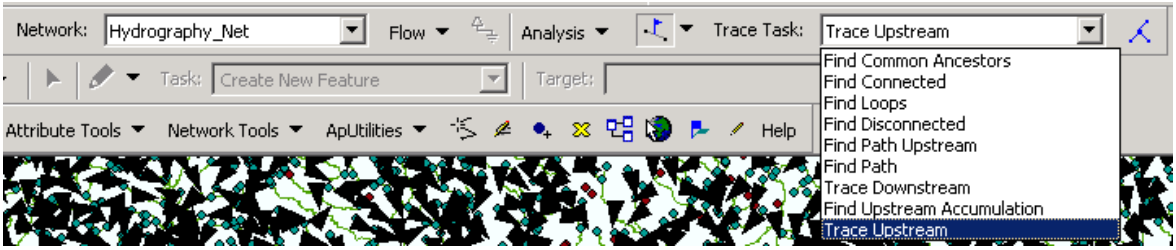
6. Set a barrier flag for the western edge of the coast by first clicking on the ***Add Edge Barrier Tool***.



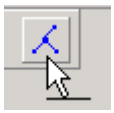
Place it at the western edge of the coastline. The position of the barrier is marked by a red X.



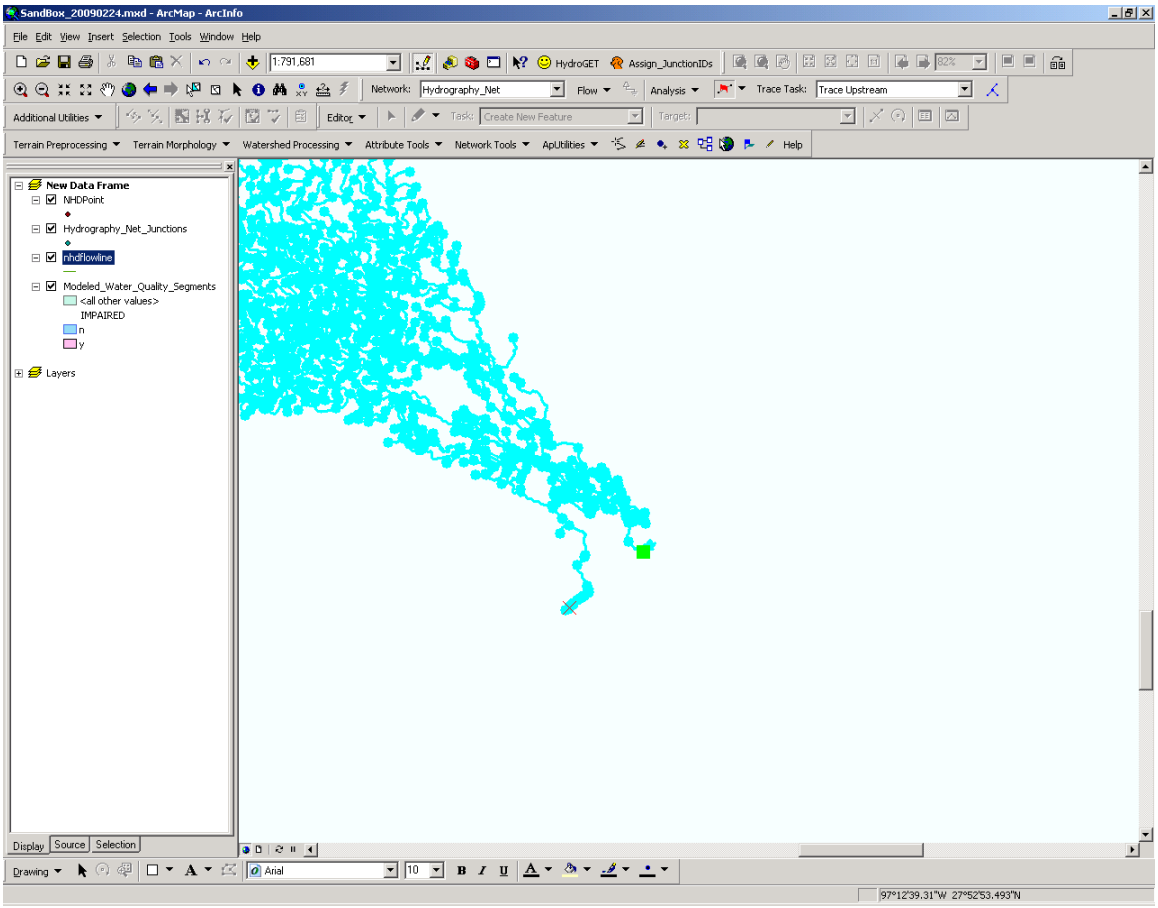
7. Select ***Trace Upstream*** from the ***Trace Task*** dropdown menu.



8. Then Click on the solve button. Be patient while it traces.



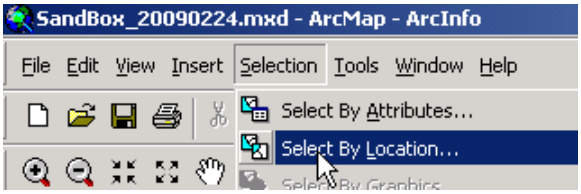
The trace will result in all the network features upstream of San Antonio Bay selected.



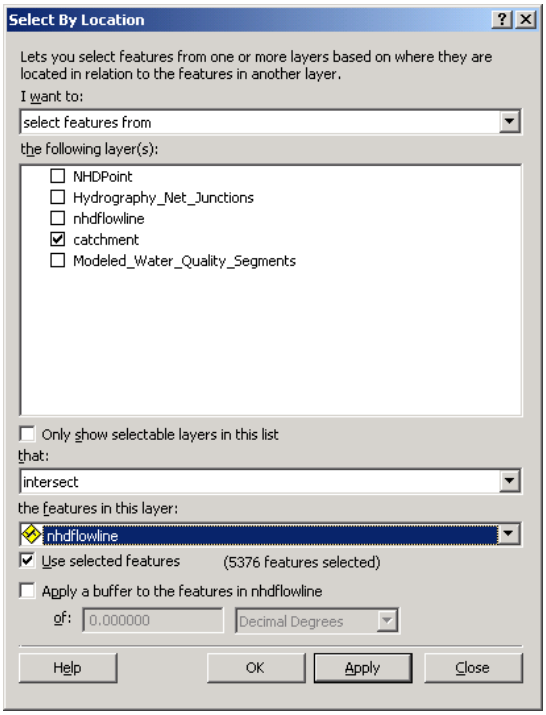
Phase VI: Extract the watershed and hydrological features that contribute to a bay

In this phase, we will extract the catchments and hydrological features (e.g. NHDflowline, NHDPoint, etc.) that contribute to a bay. In this exercise, we want to take all the catchments that are intersected by the selected flowlines and define them collectively as the San Antonio watershed.

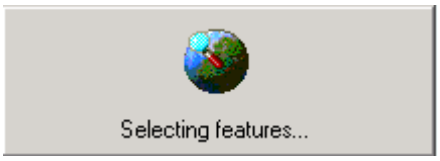
1. Let's first bring in the catchment shapefile by adding the ***catchment*** featureclass from the geodatabase to the map.
2. Next go to the main toolbar. Click on ***Selection*** and then ***Select by Location***.



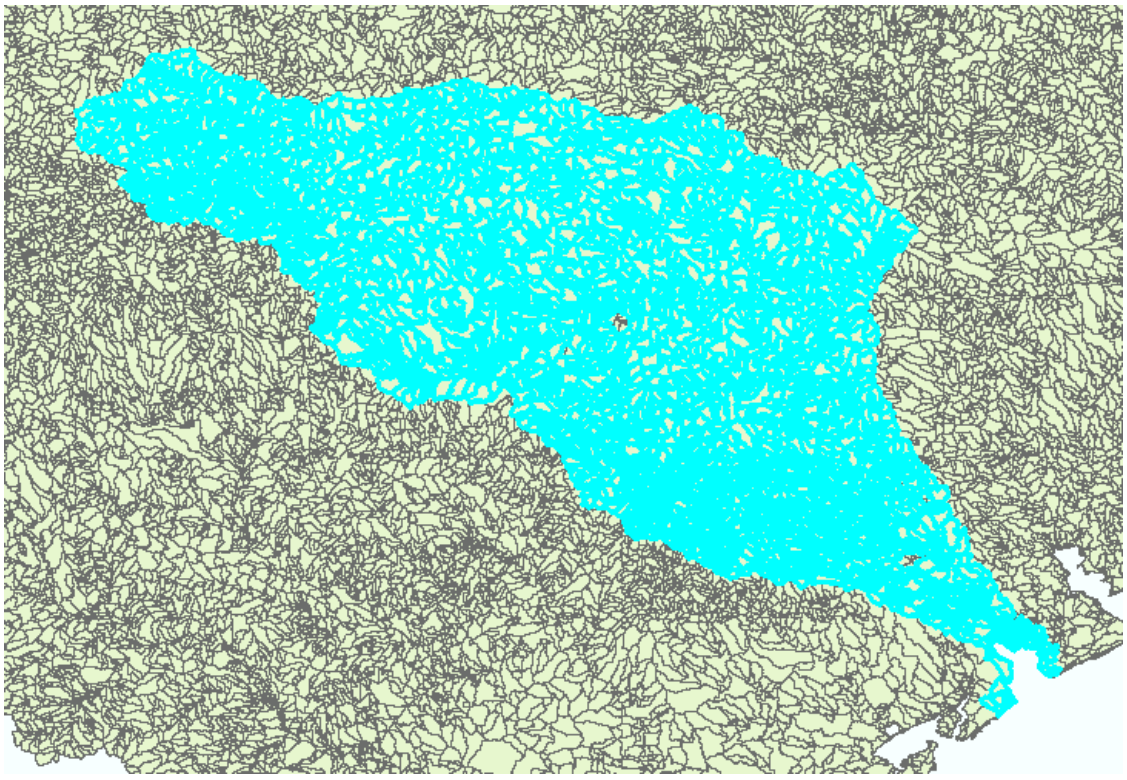
3. In the next window, specify that you want to select features from the catchment feature class that intersect with the selected nhdflowlines from the upstream trace.



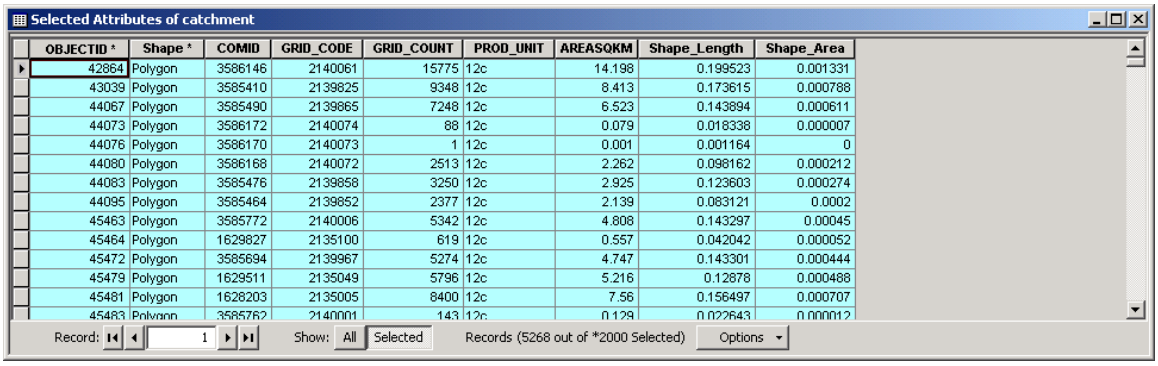
4. Hit apply and be patient.



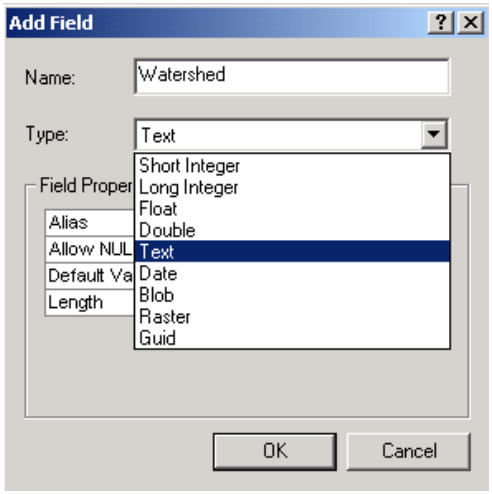
5. Once the selection is completed, the watershed of the San Antonio Bay will appear. Note, however, that there are gaps in the watershed that need to be dealt with later on.



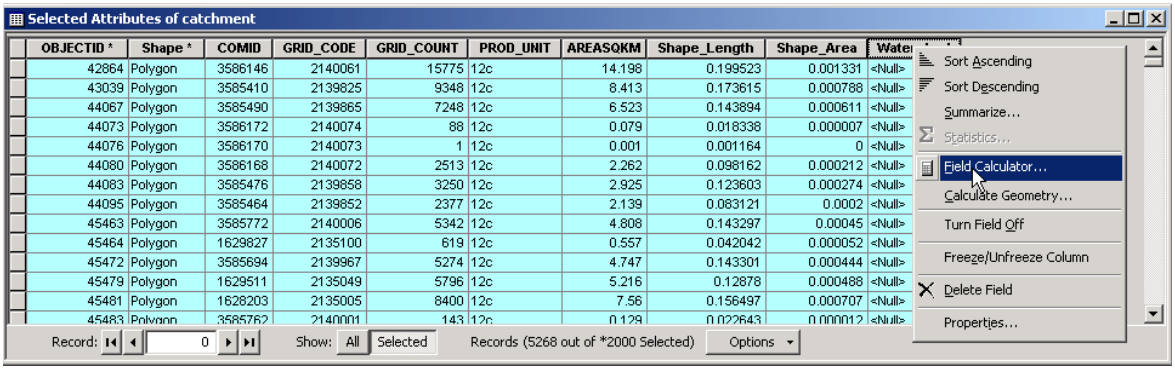
6. Let's add an identifier for the selected watersheds within the attribute table. Open the attribute table of the catchment featureclass. Hit the ***Selected*** button to show only the catchments in the watershed.



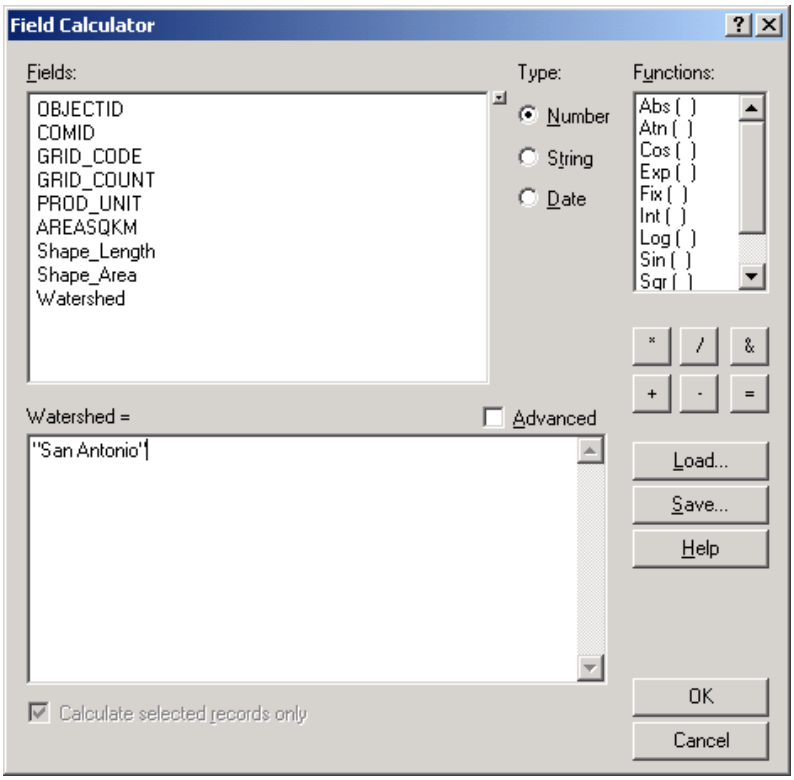
7. Add a new text field called Watershed. Click on the ***Options*** button and select ***Add Field***.



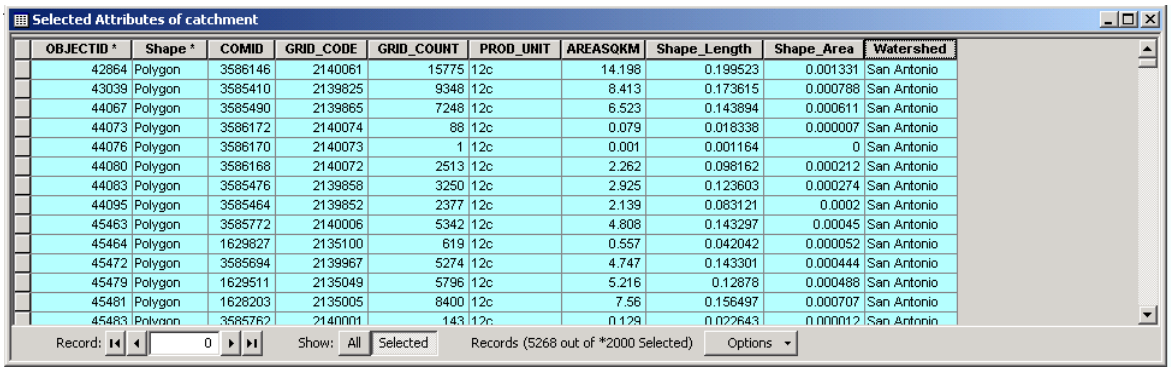
8. Perform a field calculation on the Watershed field.



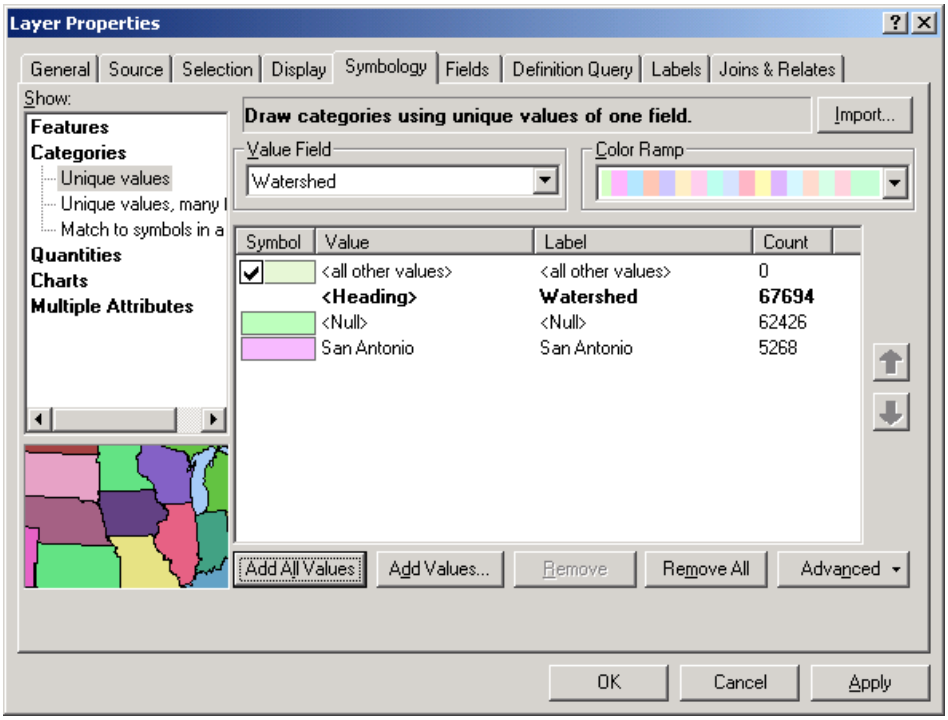
9. Type in “San Antonio” in the box.



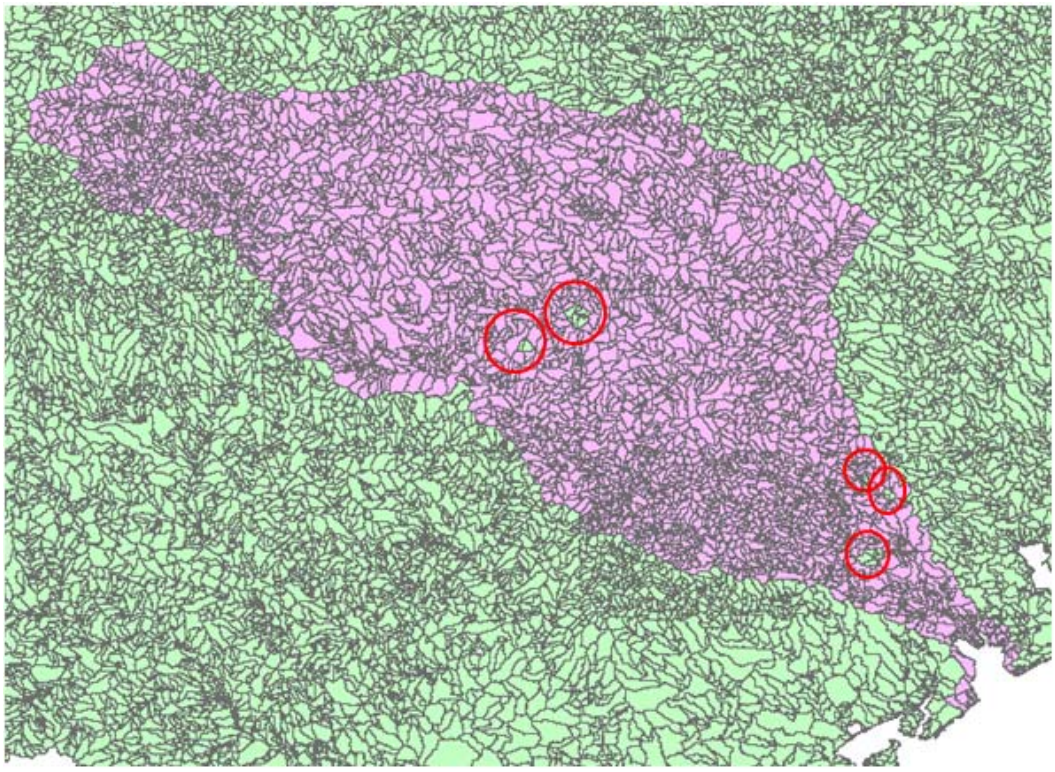
10. Hit OK. The field calculator will only give the selected features the value of “San Antonio” in the ***Watershed*** field.



11. Let's change the symbology of the catchment layer in ArcMap so that there are different colors for San Antonio catchments and the rest of the catchments.

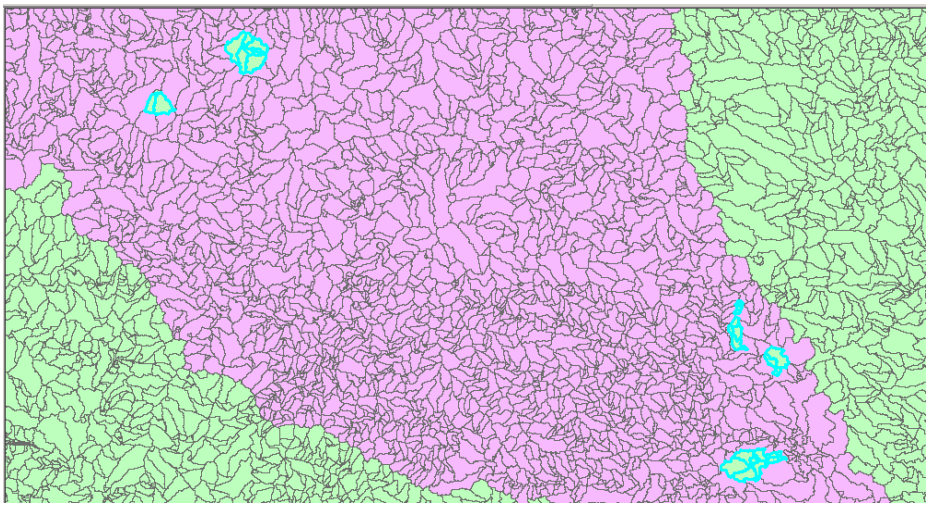


12. Once you have set the symbology, clear the selection so that you can have a better look at the San Antonio Catchment.

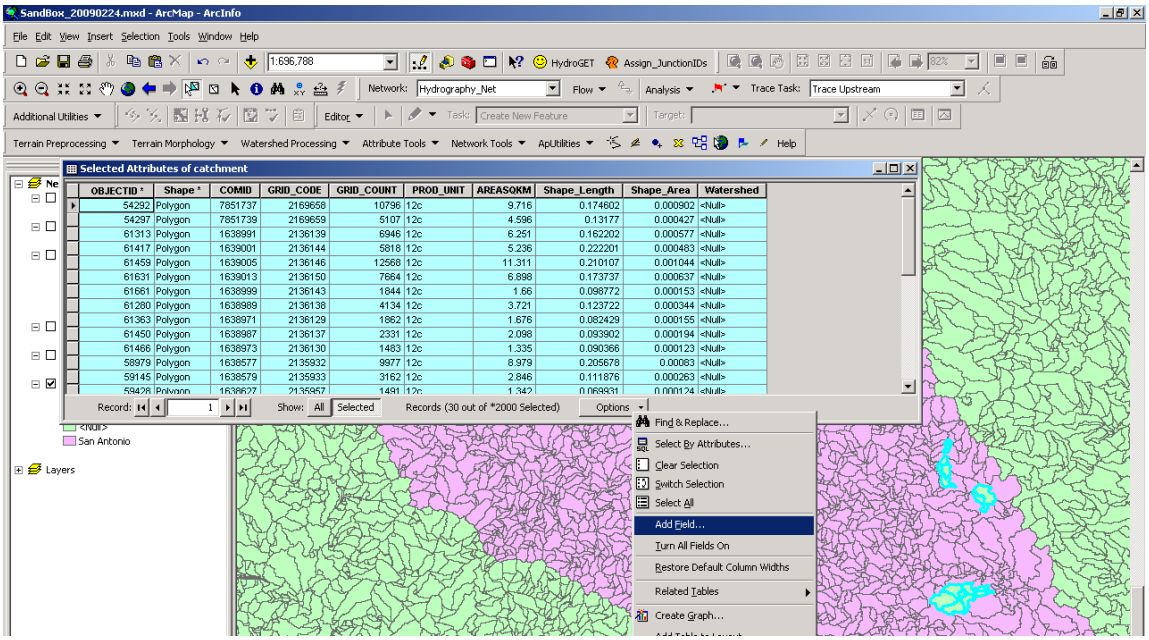


13. Notice that there are several gaps in the watershed. These catchments contain flowlines that were not connected during the upstream trace. Often this is caused by anomalies in the DEM, such as areas with no data. We should include these catchments in our watershed.

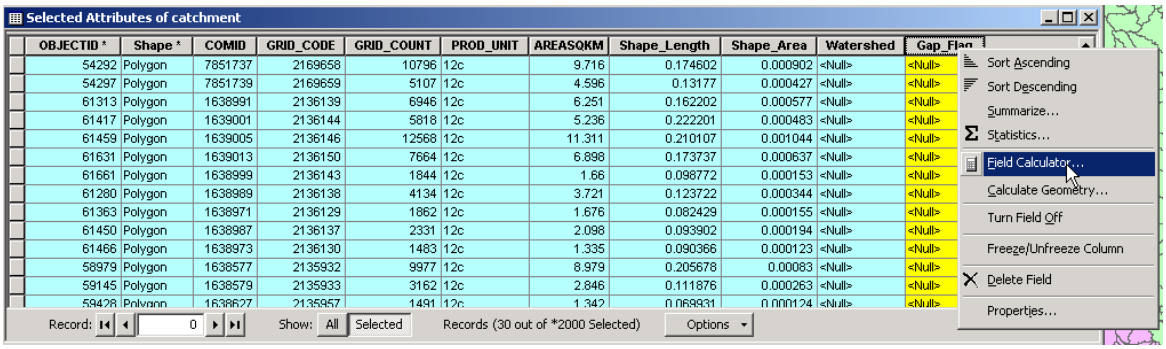
Using the selection tool, select these watersheds. Note: you may have to zoom in to properly select the watershed. Also remember to hold on to the shift key when you select so that you add to the selection instead of creating a new selection.

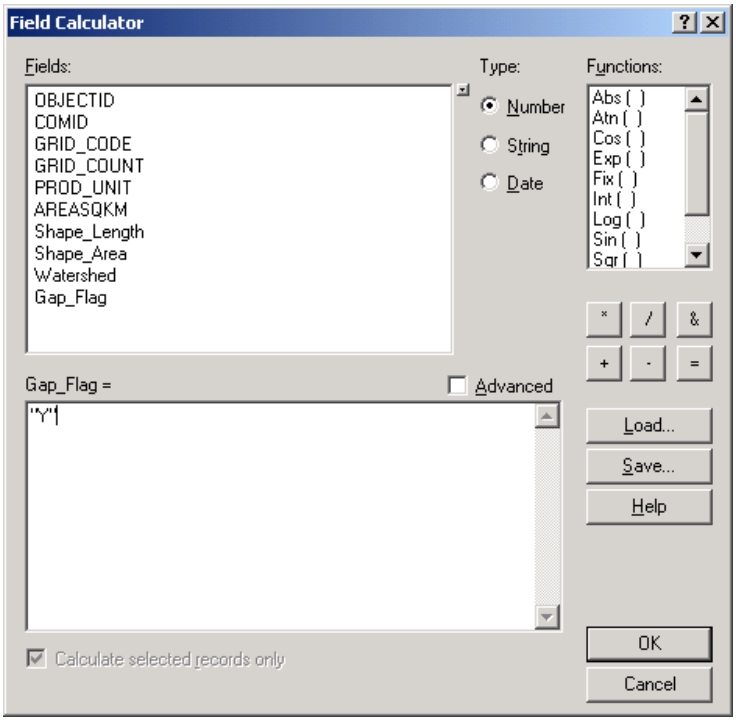


14. Let's flag these gap catchments in the attribute table. Open the attribute table and add a new text field called ***Gap_flag***.



15. Using the field calculator, give these selected catchments the value of "Y" in the ***Gap_Flag*** field.



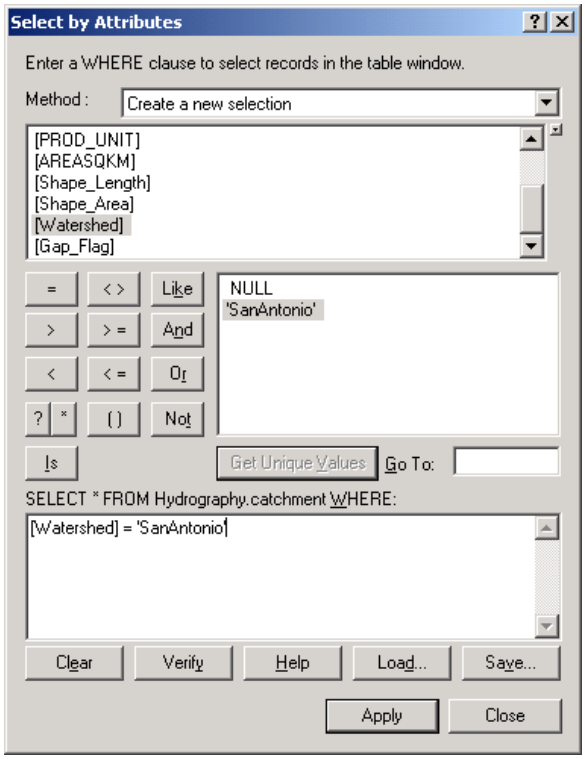


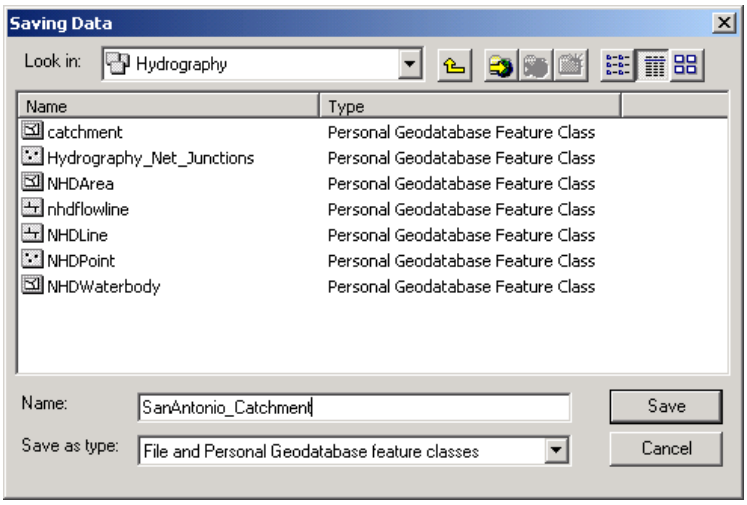
(Troubleshooting: If Arcmap gives you trouble when performing field calculations, try switching to Editor mode).

16. Since these catchments belong in the San Antonio Catchment, give them the value of "San Antonio" in the Watershed field as well.

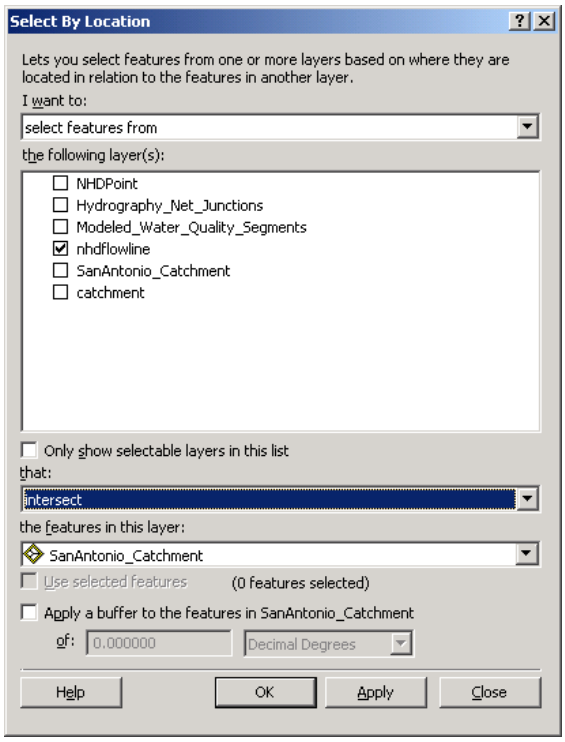
Very good. You have now identified the San Antonio watershed. We want to save this watershed in a separate featureclass.

17. Within the catchment attribute table, perform a query on the Watershed field for "San Antonio". Then export the selection to a featureclass in the geodatabase called "SanAntonio_Catchment".

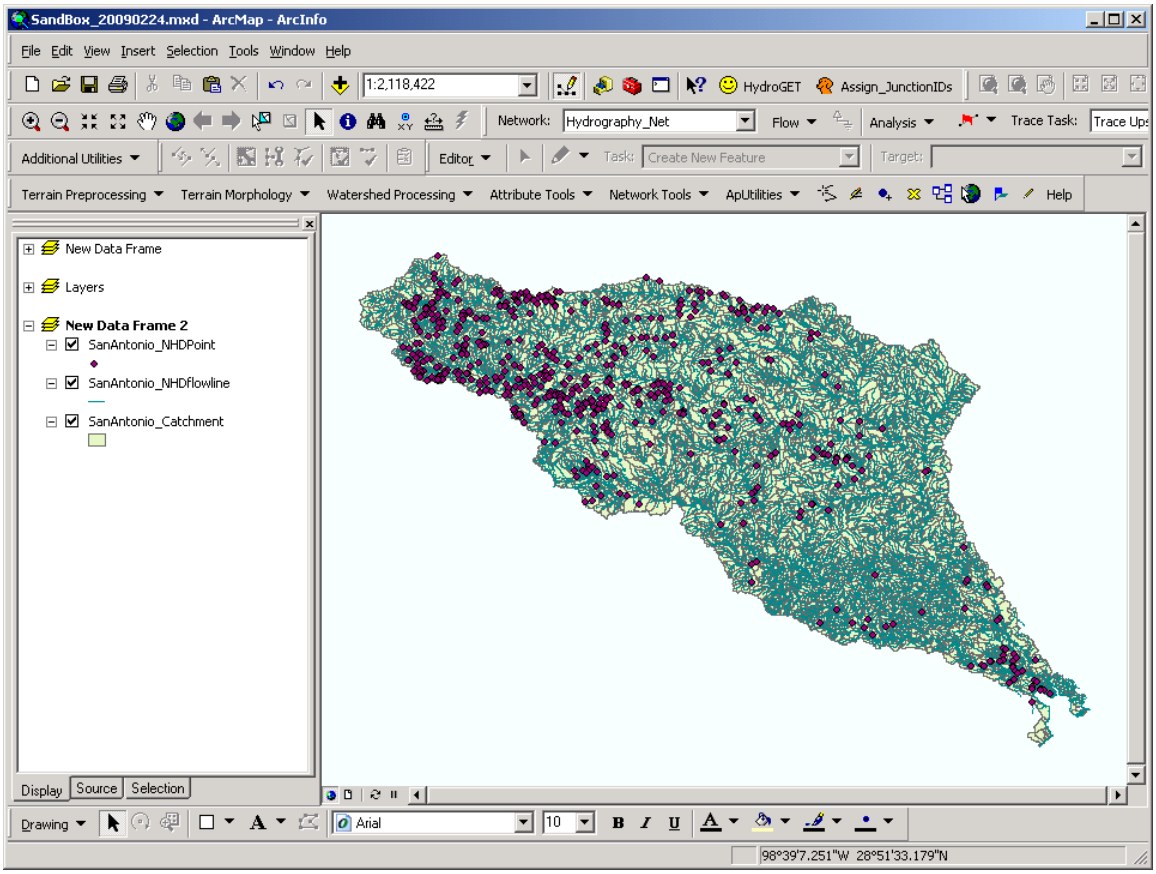




18. We want to extract all NHDflowlines and NHDPoints that fall within the San Antonio watershed. Again use the ***Select by Location*** tool and select the NHDFlowlines and NHDPoints that intersect the catchments in the watershed. Export these features to the featureclasses, SanAntonio_NHDFlowlines and SanAntonio_NHDPoints respectively.



Congratulations, you have successfully extracted NHDPlus for San Antonio Bay.



This completes Part I of the exercise.

Part II: Modifying NHDPlus features

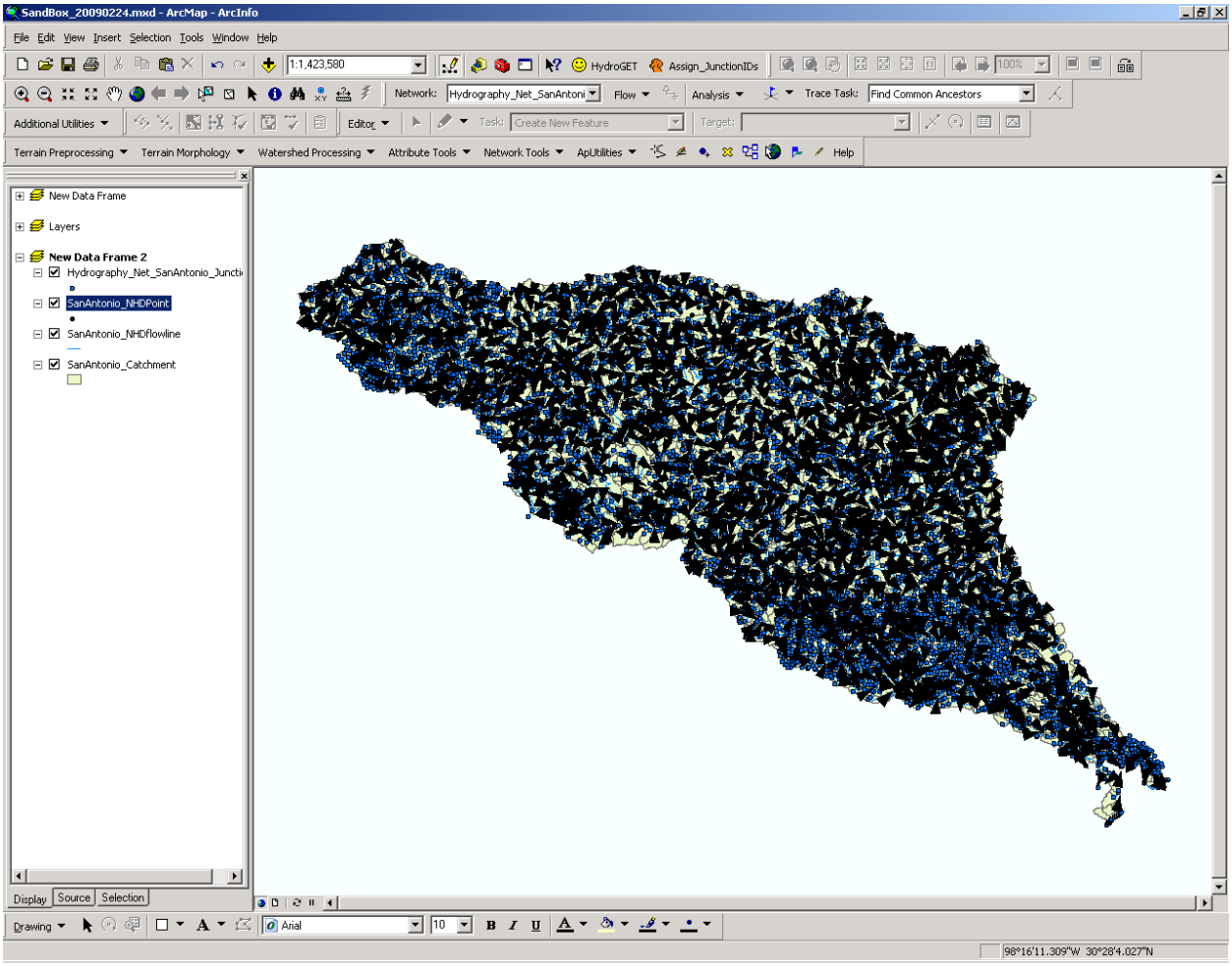
The NHDPlus features need to be modified because of the following reasons:

1. NHDPlus features may contain anomalies that have arisen from the irregularities of the source DEM. Recall that in the last part of this exercise, we identified catchments that were disconnected from the rest of the watershed. These are a result of their flow lines not connecting with the main network of the watershed. In Part II of the exercise, we will revisit these catchments.
2. NHDPlus treats the shoreline of a bay as a stream that flows towards the northeast. This is an inaccurate representation of the system and therefore needs to be removed prior to schema generation.
3. We need to set up a fictitious node in the bay for the modeling of bay dynamics.

Phase I: Recreate the geometric network for the selected waterbody

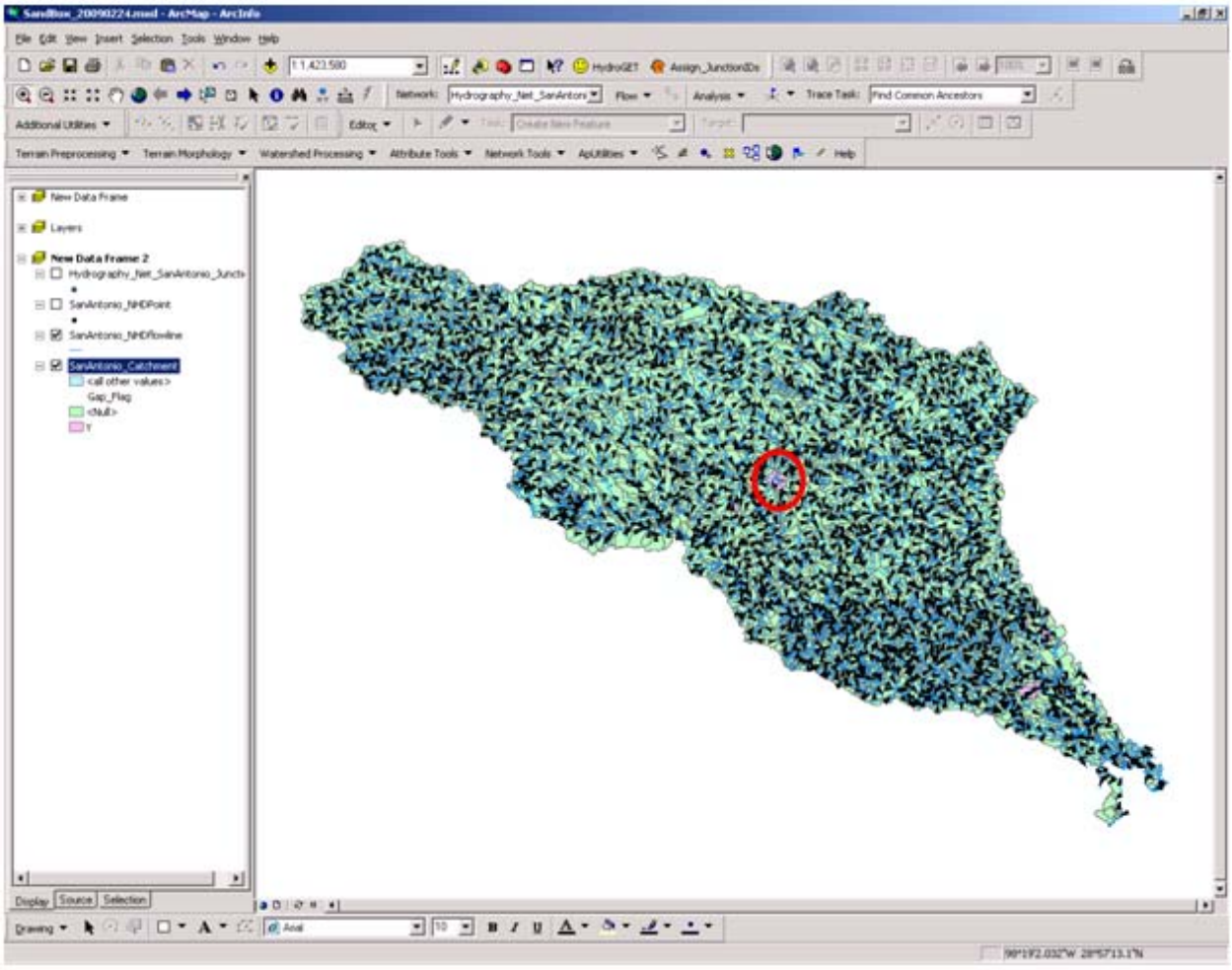
1. Let's recreate a geometric network for San Antonio Bay using the extracted features, ***SanAntonio_NHDflowline*** and ***SanAntonio_NHDpoint***. Follow the procedures in Phase III of Part I to do this. Let's call the new network ***Hydrography_net_SanAntonio***.
2. Bring the network into ArcMap and set the flow direction of the new network using the procedures in Phase IV of Part I.

3. Display the flow direction arrows (recall Phase IV of Part I).

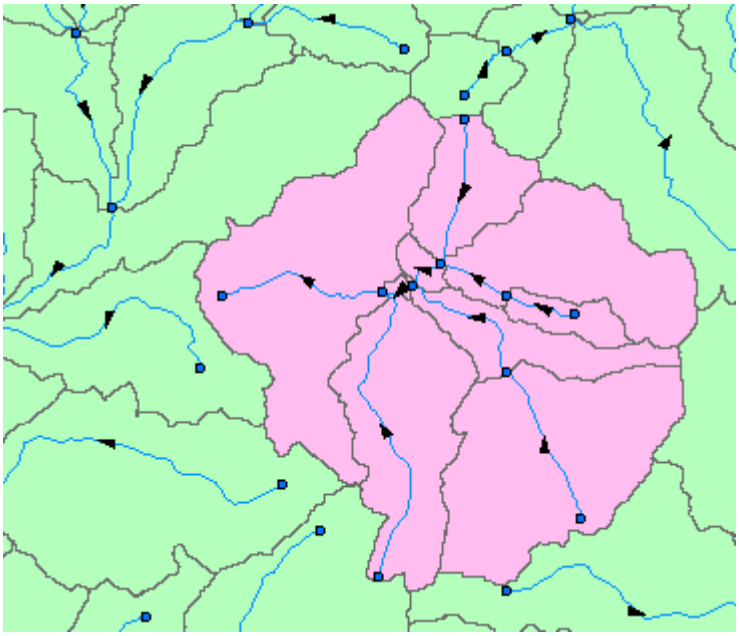


Phase II: Reconnect the flowlines for isolated catchments

1. To visualize the isolated catchments, change the symbology of ***SanAntonio_Catchment*** so that different colors are displayed for catchments with a ***Gap_flag*** value of "Y" and for those with a "<null>" value in that field (these were set in Part I of the exercise).

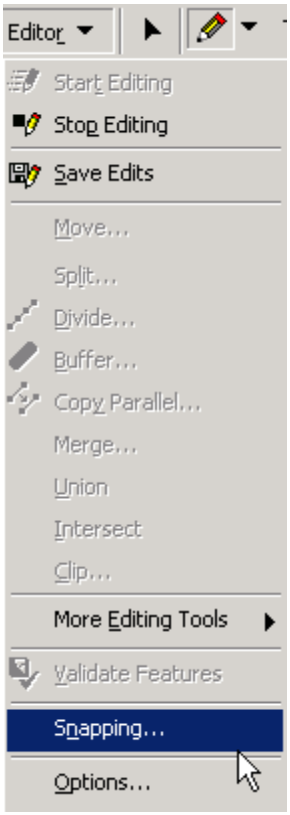


2. To demonstrate how the network can be fixed, let's zoom into one of the isolated catchments (see area circled in red above).

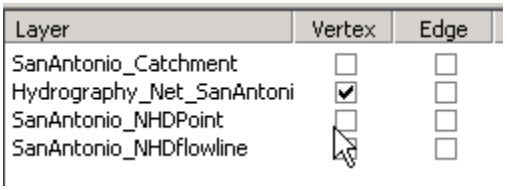


3. Notice how the network of streams within this group of catchments flows towards the westernmost junction point. However this junction point fails to connect with the main network. To connect them, we will artificially create a flowline.
4. Enter the editing mode by clicking on the ***Editor*** button and then select ***Start Editing.***

5. Let's set the snapping options so that the created features snap exactly to the hydro junction points. This is important to ensure that there are no gaps between the flowlines. Click on the ***Editor*** button and then scroll down to ***Snapping…***

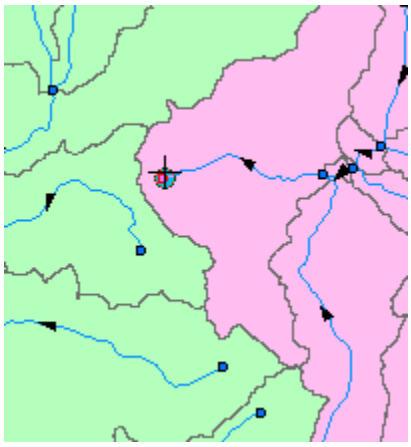


6. Put a tick on ***Vertex*** next to ***Hydrography_Net_SanAntonio***.

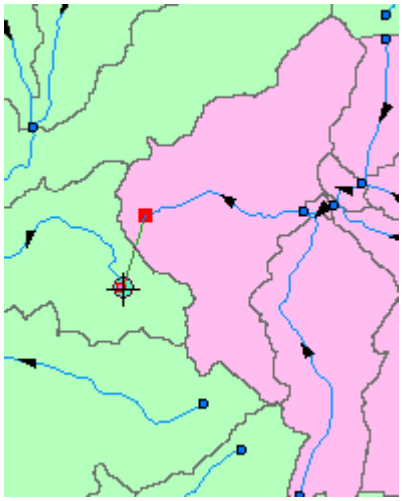


7. Make sure your editing task and target are set to ***Create New Feature*** and ***NHDFlowline_SanAntonio***, respectively.

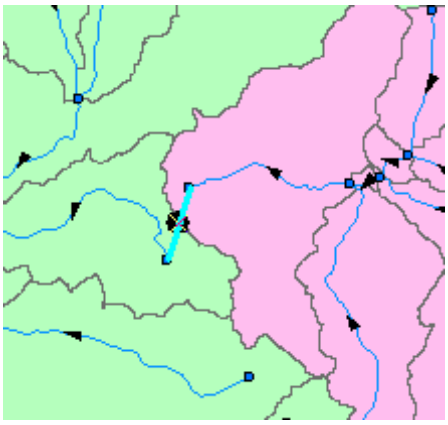
8. Click on the most downstream point within the group of isolated catchments.



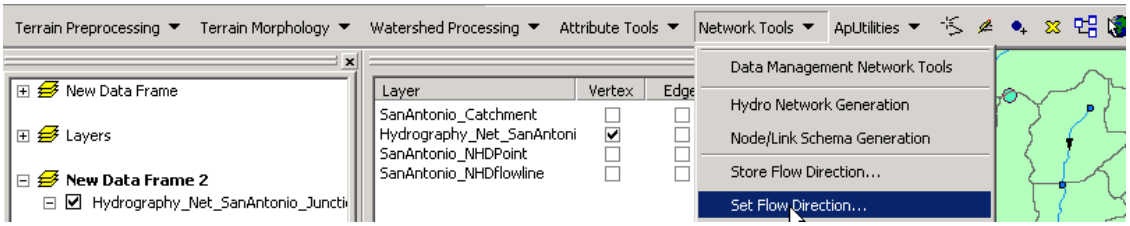
9. Then drag the line to the closest junction point in the main network.



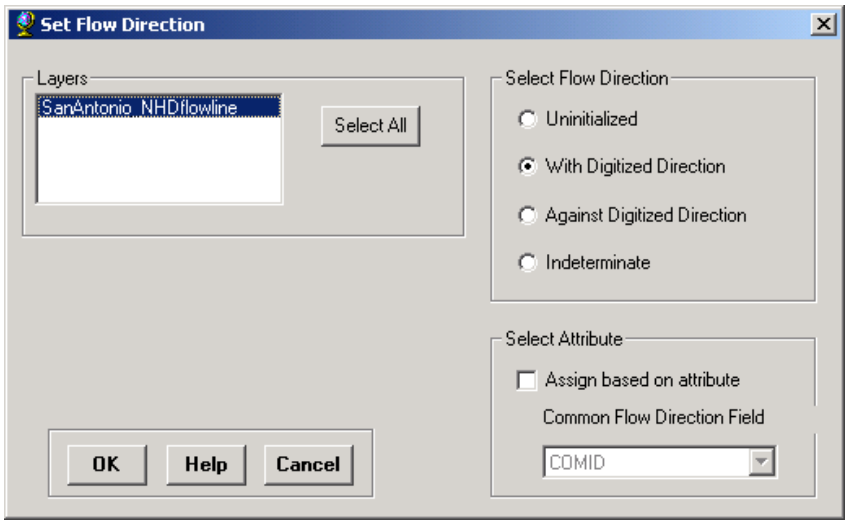
10. Note that this line does not have a flow direction set. Therefore it displays a circle instead of a flow direction arrow.



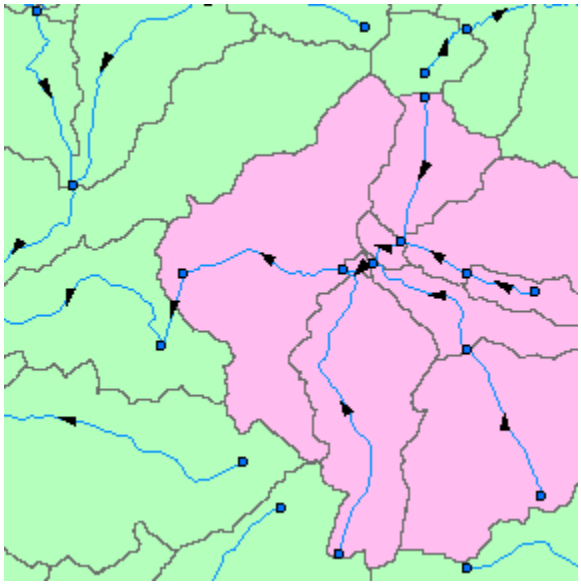
11. Let's set the flow direction by going to the ***Arc Hydro*** toolbar, click on ***Network Tools***, and select ***Set Flow Direction…***



12. Select ***SanAntonio_NHDFlowline*** as the layer and select flow direction ***With Digitized Direction***. Hit OK to continue.



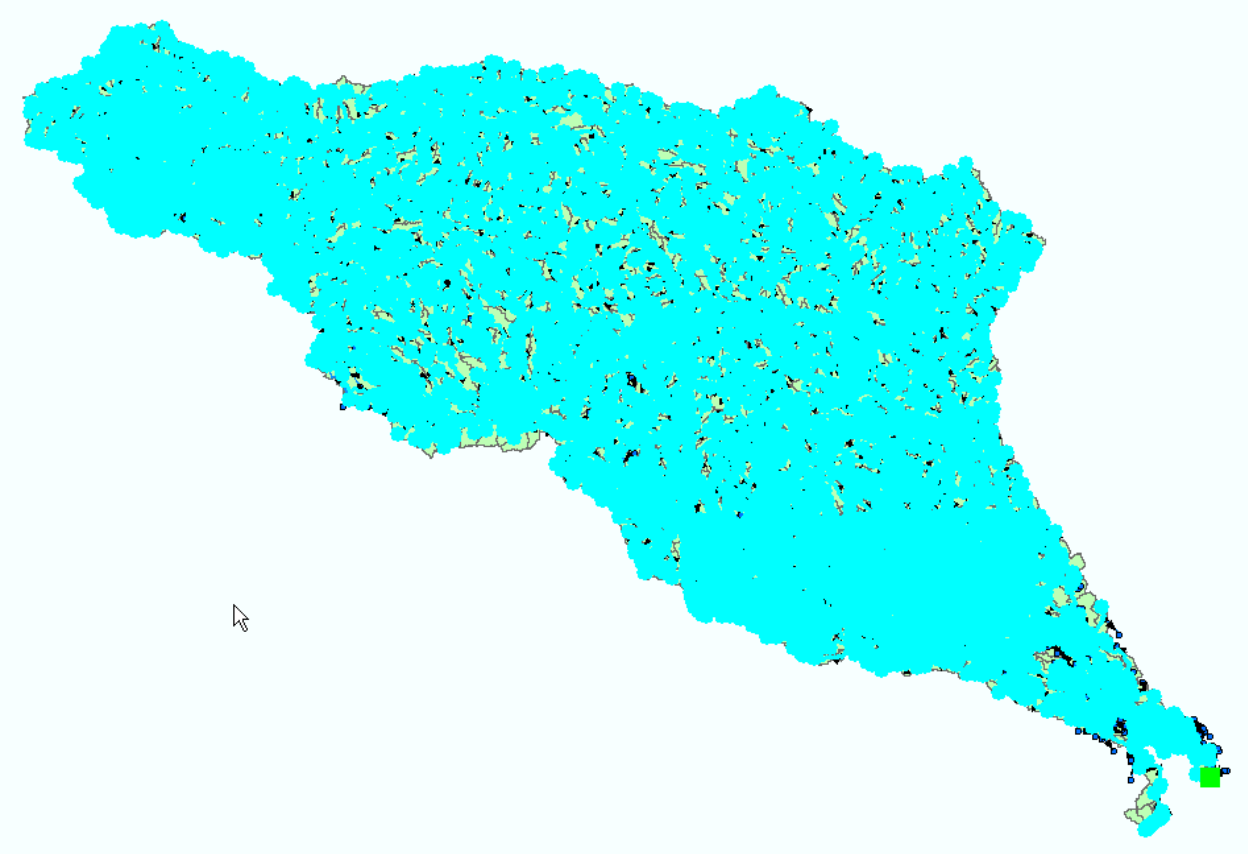
You should get a nice connected flowline now.



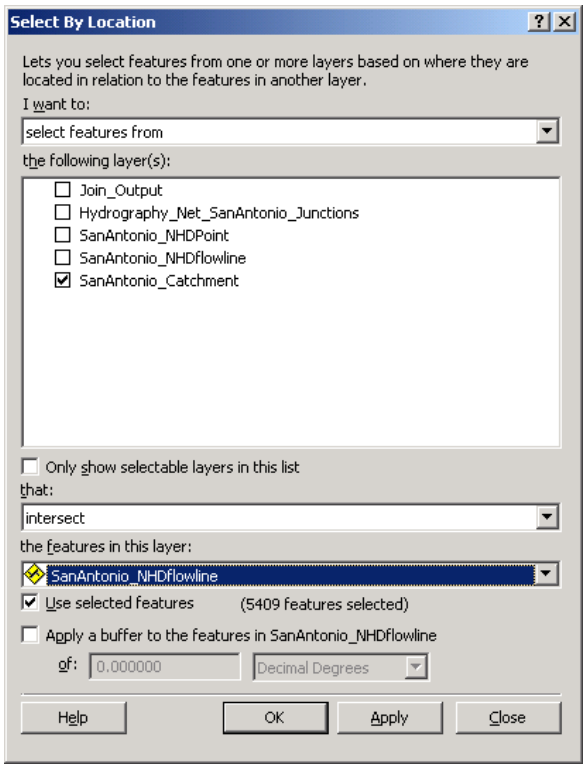
13. Repeat the above steps for the rest of the isolated catchments. Once you are done you may advance to the next phase.

Phase III: Check connections

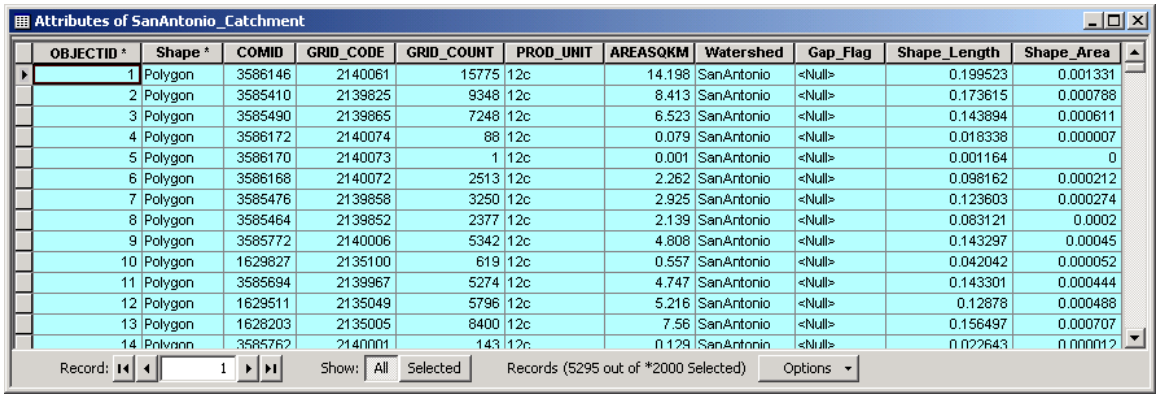
1. Perform a trace upstream according to the procedures in Part I: Phase III. (Hint: you don't need to set a barrier flag in this trace because you have removed the watersheds southwest of San Antonio Bay).



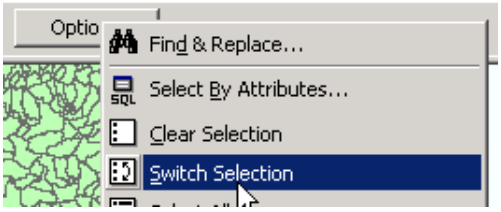
2. Perform a select by location (see Part I: Phase VI) to make sure that all the catchments are connected to the main network.



3. Once selection is complete, open the ***SanAntonio_Catchment*** table.



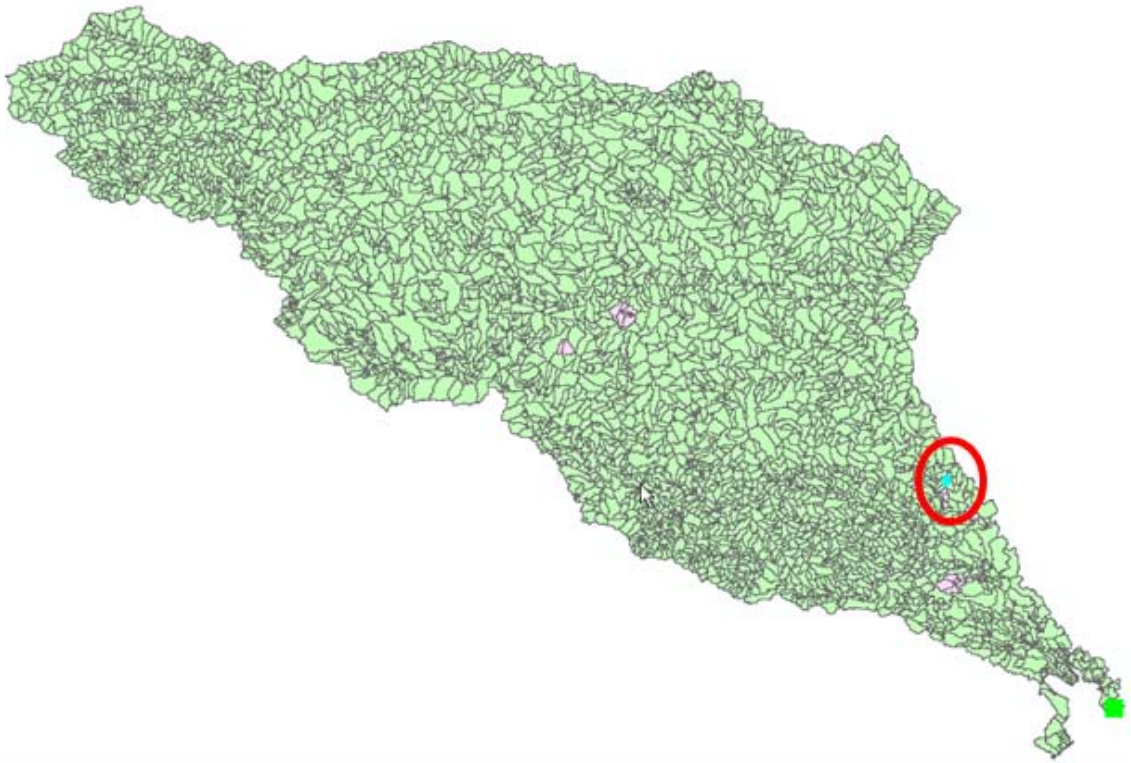
4. We want to find out which catchments have not been selected. So let's switch the selection by hitting the ***Options*** button, and select ***Switch Selection***.



Selected Attributes of SanAntonio_Catchment

OBJECTID *	Shape *	COMID	GRID_CODE	GRID_COUNT	PROD_UNIT	AREASQKM	Watershed	Gap_Flag	Shape_Length	Shape_Area
3917	Polygon	1638231	2135759	641	12c	0.577	SanAntonio	Y	0.038753	0.000053
3936	Polygon	24677538	2185228	228	12c	0.205	SanAntonio	Y	0.025876	0.000019
3940	Polygon	1638261	2135774	1023	12c	0.921	SanAntonio	Y	0.057193	0.000085
3944	Polygon	1638229	2135758	84	12c	0.076	SanAntonio	Y	0.020082	0.000007
3971	Polygon	24677540	2185229	649	12c	0.584	SanAntonio	Y	0.040488	0.000054

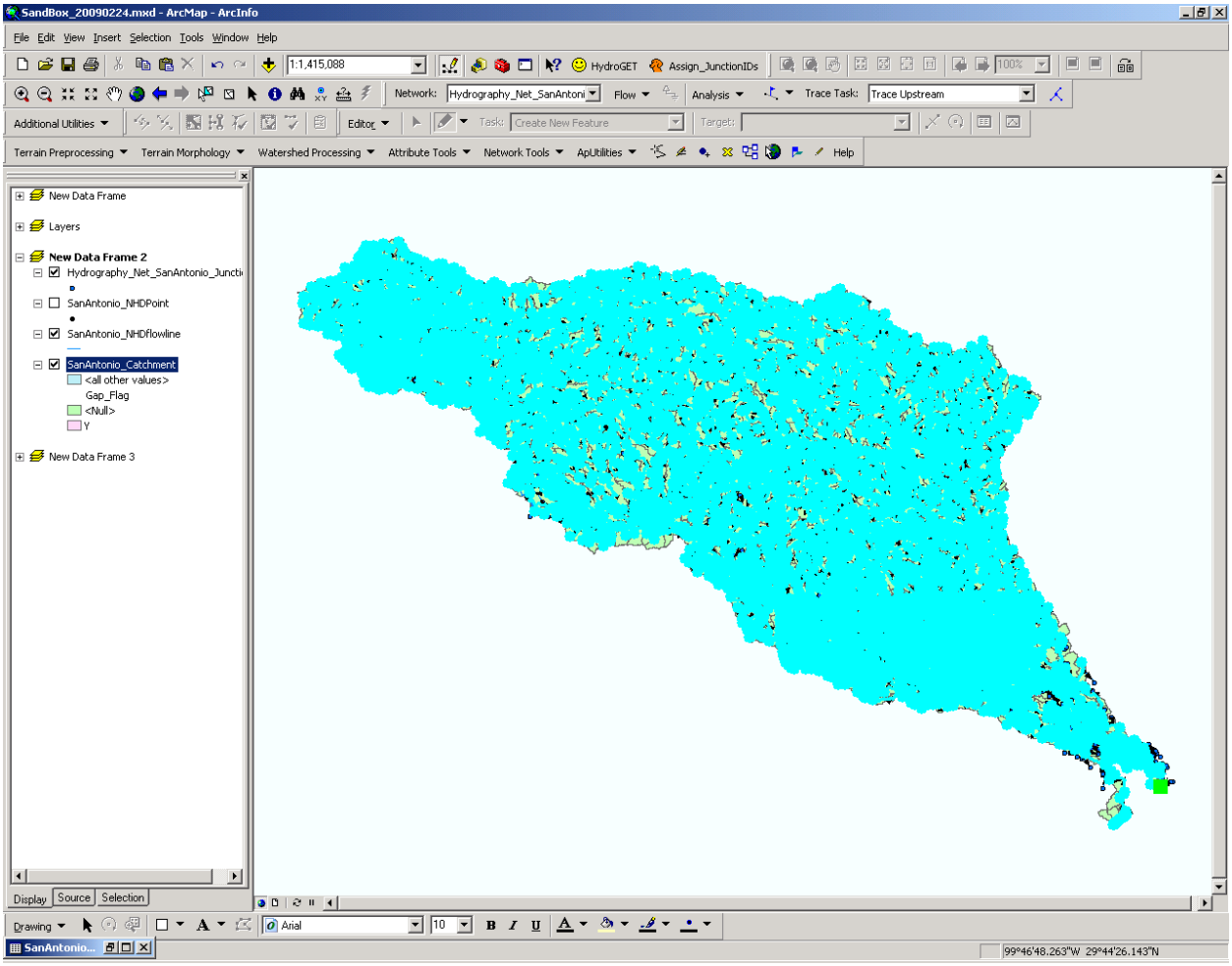
5. On the map, inactivate all layers except for ***SanAntonio_Catchment***. This way the remaining isolated catchments can be visualized.



6. Repeat Phase II to reconnect flowlines to these catchments. Repeat Phase III to check for remaining isolated catchments. Do this until all catchments are connected. Then move on to Phase IV.

Phase IV: Extract final version of NHDflowlines for the watershed

1. Perform an upstream trace as per Part I: Phase V.



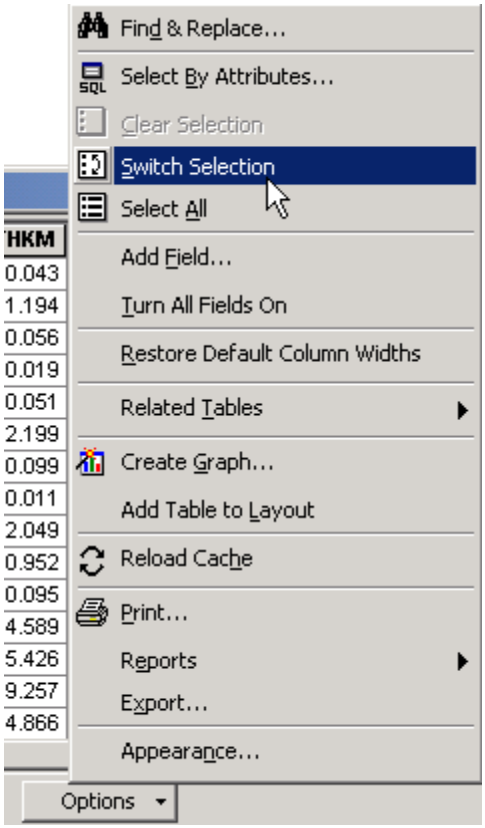
2. Notice that the trace does not include all the flowlines with ***SanAntonio_Catchments***. Most of the unselected flowlines are isolated ditches or canals that do not flow to the main network of the watershed.

Since we have ensured in Phase III that the selected flowlines can connect all the catchments in the watershed, we can disregard these unselected flowlines when creating the schematic network. Let's delete the unselected flowlines from the flowline featureclass.

3. Switch to ***Editor*** mode.

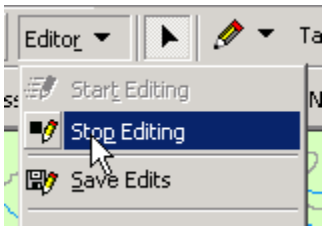
4. Make sure that you have ***SanAntonio_NHDFlowlines*** as the target layer.

5. Open the attribute table of ***SanAntonio_NHDFlowline.*** Click on the ***Options*** button and select ***Switch Selection***. This will select the previously unselected flowlines.



6. Delete the flowlines from the attribute table simply by hitting delete.

7. Stop and save the edits.



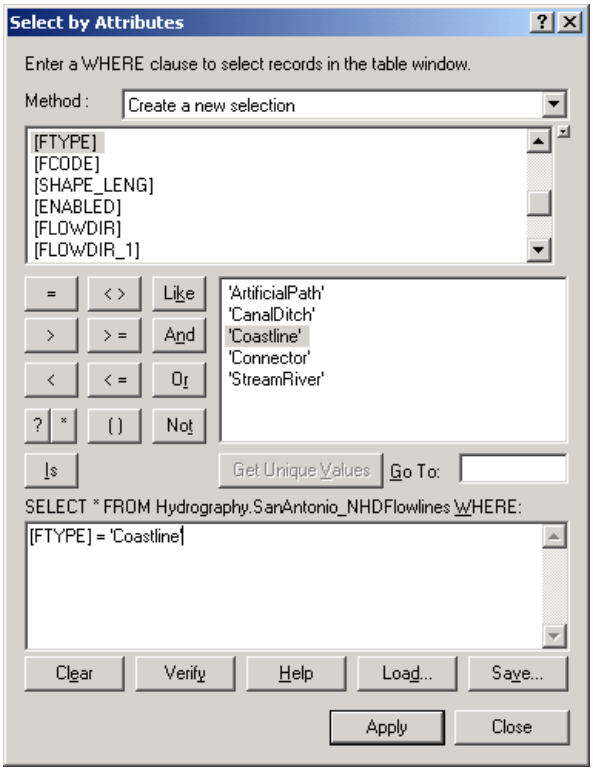
Phase VI: Remove the shoreline from the flowline featureclass

Recall that NHDPlus represents the shoreline as a stream that flows towards the northeast. We do not want this inaccurate representation to be carried into the generated schematic network. Schema networks that lead to a shoreline should end there instead of propagating along. For this reason, we will remove the shoreline ***SanAntonio_NHDFlowlines_Final.***

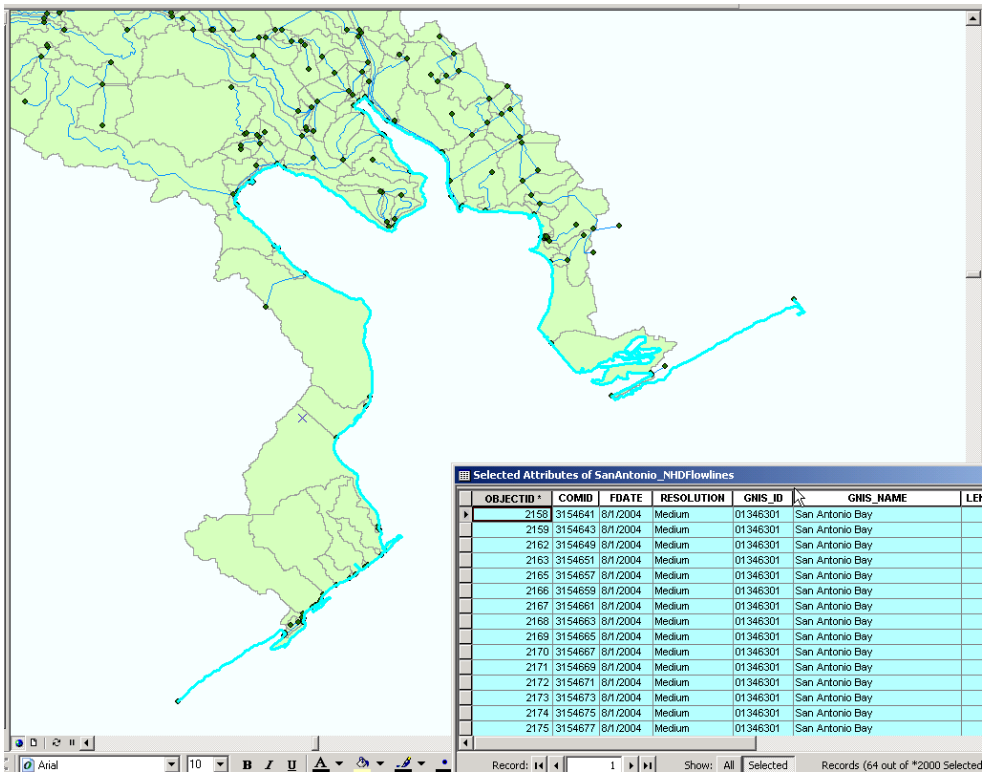
1. Switch to ***Editor*** mode.

2. Make sure that you have ***SanAntonio_NHDFlowlines*** as the target layer.

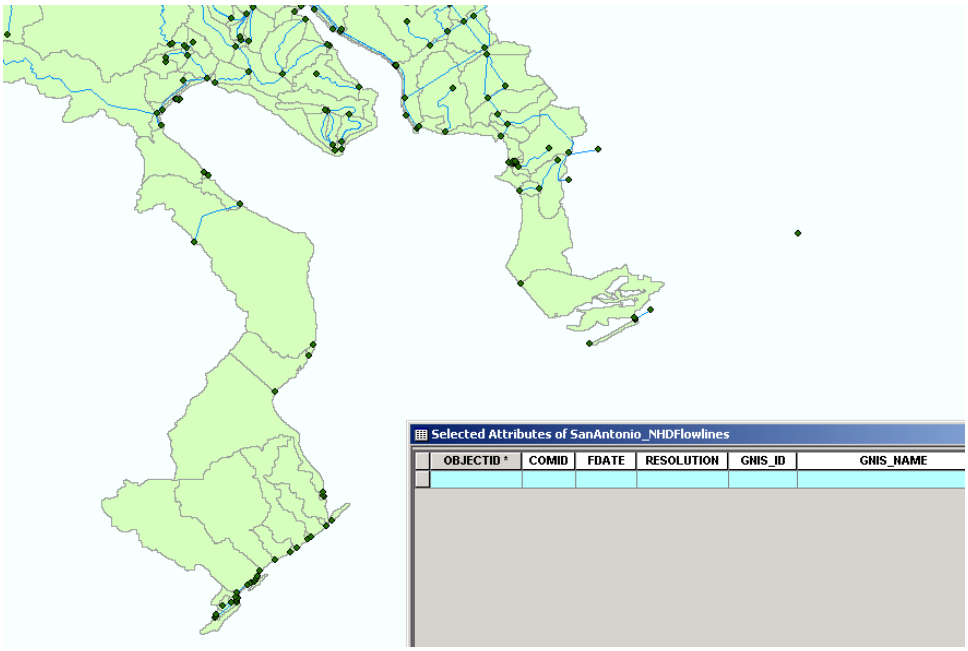
3. Open up the attribute table of ***SanAntonio_NHDFlowlines*** and perform a query on the coastline as follows.



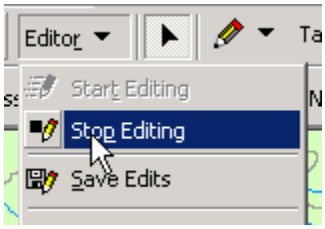
This will select out the coastline of San Antonio Bay as shown.



4. Delete the selected featureclasses from the attribute table simply by hitting delete.



5. Stop and save the edits.



Phase VII: Add a fictitious node in the bay and connect it to the rest of the flowlines.

We will add a node inside a bay so that we can model bay dynamics in the schematic network.

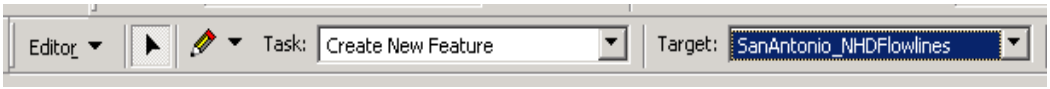
1. Switch to ***Editor*** mode.

2. Make sure that you have ***SanAntonio_Junctions*** as the target layer.

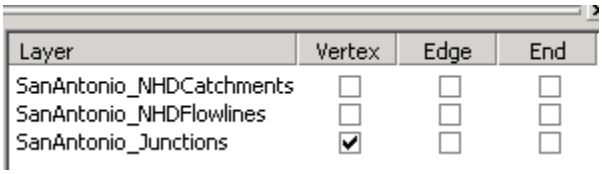
3. Click on the sketch tool  and click on a point in the bay to create a junction as shown.

4. Stop editing and save edits.

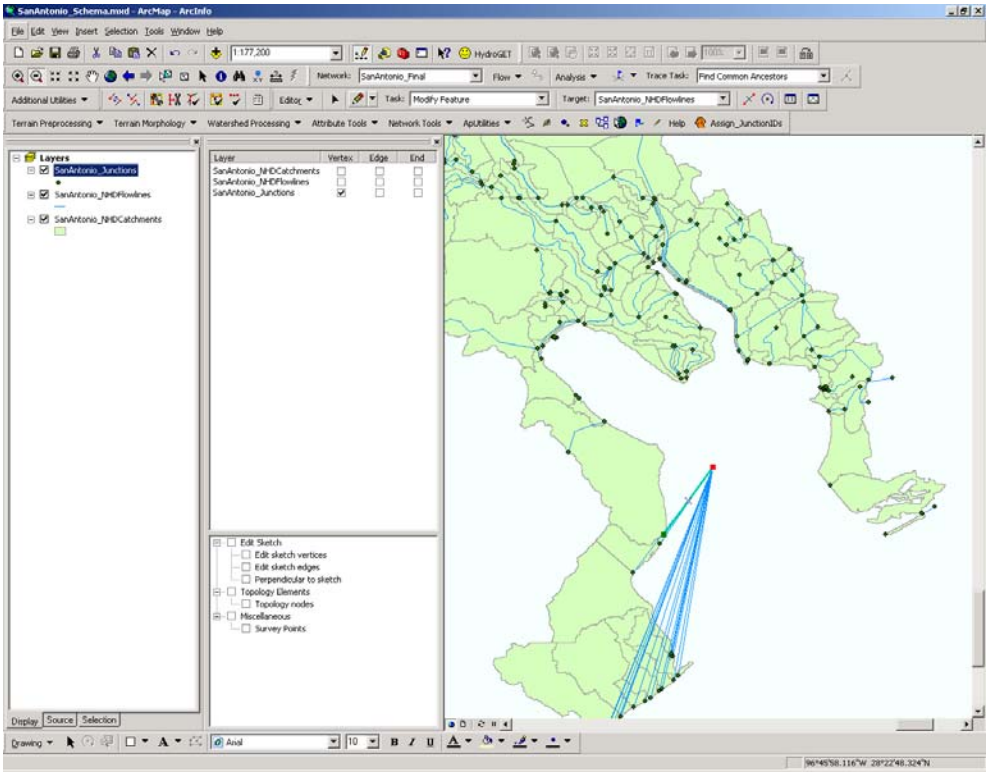
   Next let's edit the ***SanAntonio_NHDFlowlines***.



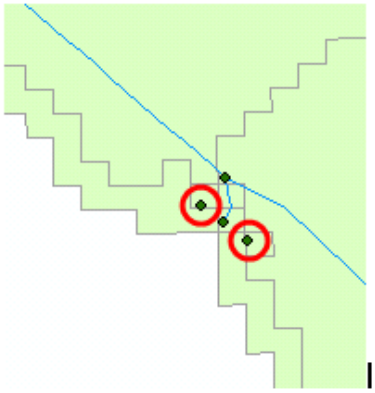
5. Make sure you set your snapping options so that the vertices match up with ***SanAntonio_Junctions***.



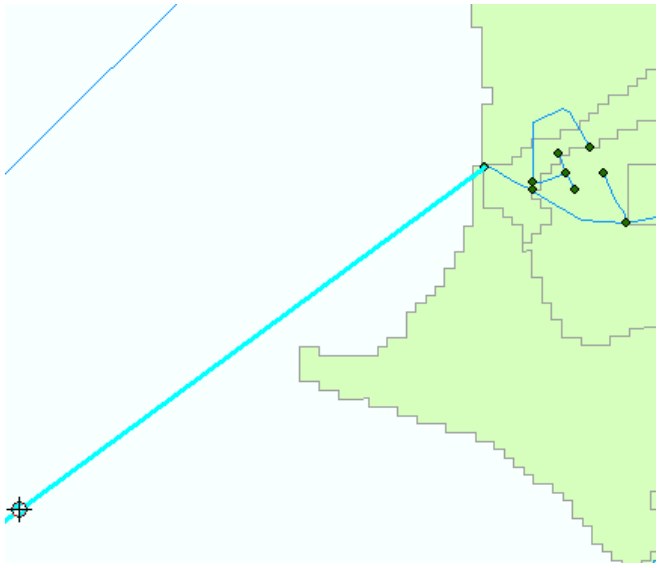
6. Start connecting the nodes on the coastline to the bay node one by one. Make sure you click on the **coastline nodes first and the bay node second** to preserve the direction.



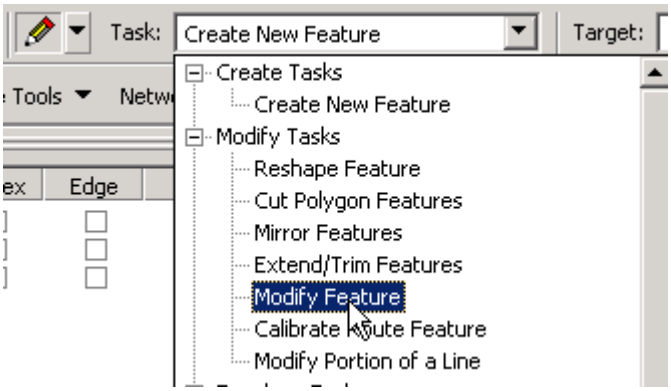
When connecting nodes, you can use your judgment to decide which nodes to include. For instance, nodes that are outlets to minute watersheds are probably not worth connecting (see ones circled in red below) because they do not add more accuracy to the model.



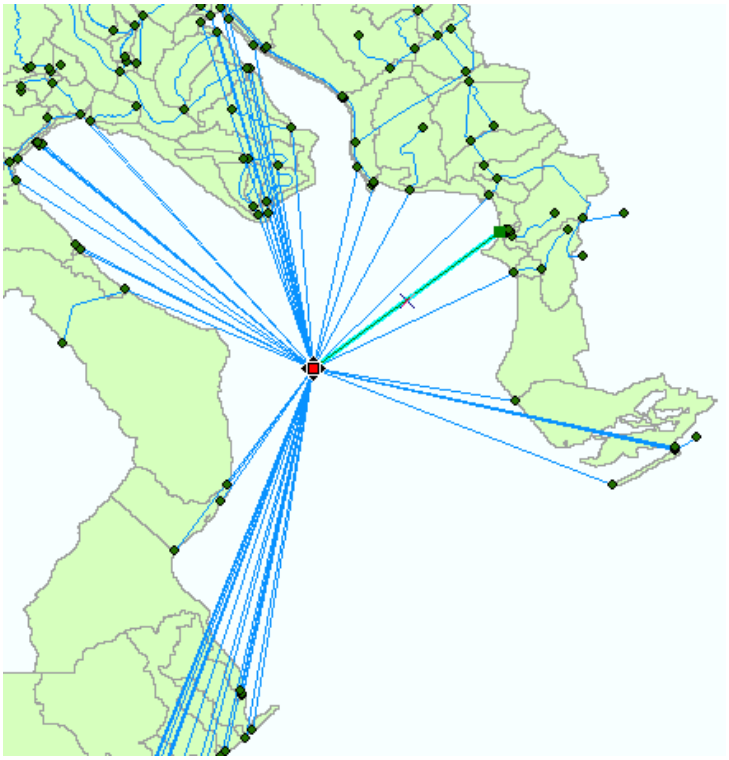
A little trick: in instances where you have to zoom in to such a small scale that you cannot see both the bay and coastal node in the same frame. You can first create a line that extends out from the coastal node and then zoom out to where you can see the bay node.



7. Switch to modify feature mode and then select the line you just created with the select tool  .



8. Pull the dangling node to the bay node and click it.



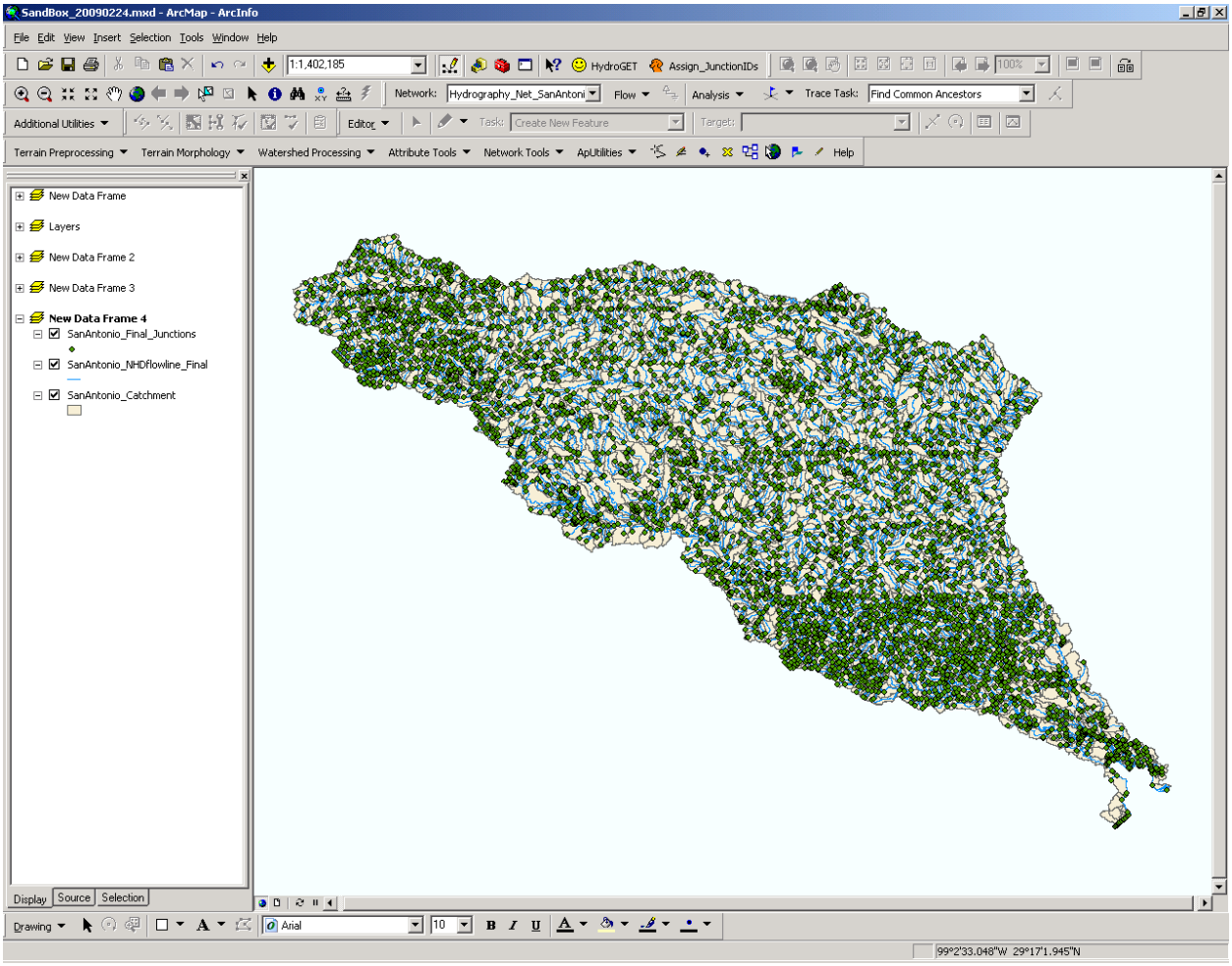
9. Once you have finished connecting the nodes, stop editing and save your edits.

10. Regenerate a new geometric network and set its flow direction as per instructions in Part I:Phase III and Phase IV. Call this new network SanAntonio_Final.

Part III: Making NHDPlus compatible with Arc Hydro

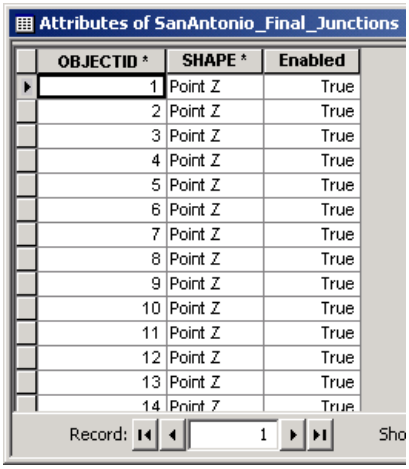
Phase I: Add necessary fields to the watershed featureclasses

1. After you have created a new geometric network with ***SanAntonio_NHDFlowlines_Final*** and ***SanAntonio_NHDPoints***, bring it into ArcMap. Set the flow direction of the network as per Part I: Phase IV. Also bring in ***SanAntonio_Catchment***. We are going to establish the connectivity among all these three featureclasses.



2. Let's inspect the attribute tables of these three featureclasses:

a. Junction featureclass:

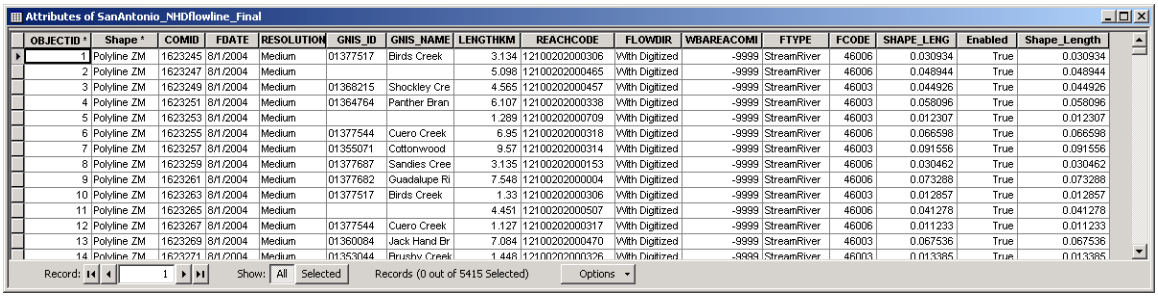


Attributes of SanAntonio_Final_Junctions

OBJECTID *	SHAPE *	Enabled
1	Point Z	True
2	Point Z	True
3	Point Z	True
4	Point Z	True
5	Point Z	True
6	Point Z	True
7	Point Z	True
8	Point Z	True
9	Point Z	True
10	Point Z	True
11	Point Z	True
12	Point Z	True
13	Point Z	True
14	Point Z	True

Record: 1 Sho

b. Flowline featureclass:

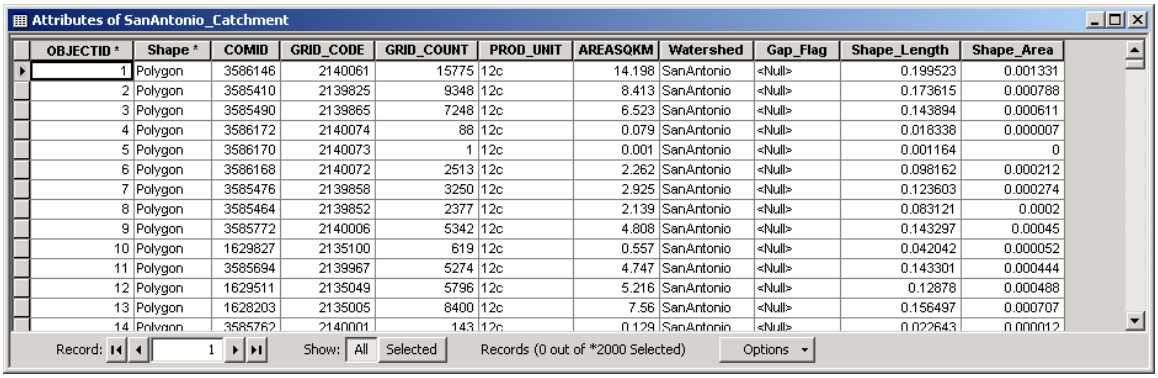


Attributes of SanAntonio_NHDflowline_Final

OBJECTID *	Shape *	COMID	FDATE	RESOLUTION	GNIS_ID	GNIS_NAME	LENGTHKM	REACHCODE	FLOWDIR	WBAREACOMI	FTYPE	FCODE	SHAPE_LENG	Enabled	Shape_Length
1	Polyline ZM	1623245	8/1/2004	Medium	01377517	Birds Creek	3.134	12100202000306	With Digitized	-9999	StreamRiver	46006	0.030934	True	0.030934
2	Polyline ZM	1623247	8/1/2004	Medium			5.098	12100202000465	With Digitized	-9999	StreamRiver	46006	0.048944	True	0.048944
3	Polyline ZM	1623249	8/1/2004	Medium	01368215	Shockley Cre	4.565	12100202000457	With Digitized	-9999	StreamRiver	46003	0.044926	True	0.044926
4	Polyline ZM	1623251	8/1/2004	Medium	01364764	Panther Bran	6.107	12100202000338	With Digitized	-9999	StreamRiver	46003	0.058096	True	0.058096
5	Polyline ZM	1623253	8/1/2004	Medium			1.289	12100202000709	With Digitized	-9999	StreamRiver	46003	0.012307	True	0.012307
6	Polyline ZM	1623255	8/1/2004	Medium	01377544	Cuero Creek	6.95	12100202000318	With Digitized	-9999	StreamRiver	46006	0.066598	True	0.066598
7	Polyline ZM	1623257	8/1/2004	Medium	01355071	Cottonwood	9.57	12100202000314	With Digitized	-9999	StreamRiver	46003	0.091556	True	0.091556
8	Polyline ZM	1623259	8/1/2004	Medium	01377687	Sandies Cree	3.135	12100202000153	With Digitized	-9999	StreamRiver	46006	0.030462	True	0.030462
9	Polyline ZM	1623261	8/1/2004	Medium	01377682	Guadalupe Ri	7.548	12100202000004	With Digitized	-9999	StreamRiver	46006	0.073288	True	0.073288
10	Polyline ZM	1623263	8/1/2004	Medium	01377517	Birds Creek	1.33	12100202000306	With Digitized	-9999	StreamRiver	46003	0.012857	True	0.012857
11	Polyline ZM	1623265	8/1/2004	Medium			4.451	12100202000507	With Digitized	-9999	StreamRiver	46006	0.041278	True	0.041278
12	Polyline ZM	1623267	8/1/2004	Medium	01377544	Cuero Creek	1.127	12100202000317	With Digitized	-9999	StreamRiver	46006	0.011233	True	0.011233
13	Polyline ZM	1623269	8/1/2004	Medium	01360084	Jack Hand Br	7.084	12100202000470	With Digitized	-9999	StreamRiver	46003	0.067536	True	0.067536
14	Polyline ZM	1623271	8/1/2004	Medium	01353044	Brushy Creek	1.448	12100202000326	With Digitized	-9999	StreamRiver	46003	0.013385	True	0.013385

Record: 1 Show: All Selected Records (0 out of 5415 Selected) Options

c. Catchment featureclass:



Attributes of SanAntonio_Catchment

OBJECTID *	Shape *	COMID	GRID_CODE	GRID_COUNT	PROD_UNIT	AREASQKM	Watershed	Gap_Flag	Shape_Length	Shape_Area
1	Polygon	3586146	2140061	15775	12c	14.198	SanAntonio	<Null>	0.199523	0.001331
2	Polygon	3585410	2139825	9348	12c	8.413	SanAntonio	<Null>	0.173615	0.000788
3	Polygon	3585490	2139865	7248	12c	6.523	SanAntonio	<Null>	0.143894	0.000611
4	Polygon	3586172	2140074	88	12c	0.079	SanAntonio	<Null>	0.018338	0.000007
5	Polygon	3586170	2140073	1	12c	0.001	SanAntonio	<Null>	0.001164	0
6	Polygon	3586168	2140072	2513	12c	2.262	SanAntonio	<Null>	0.098162	0.000212
7	Polygon	3585476	2139858	3250	12c	2.925	SanAntonio	<Null>	0.123603	0.000274
8	Polygon	3585464	2139852	2377	12c	2.139	SanAntonio	<Null>	0.083121	0.0002
9	Polygon	3585772	2140006	5342	12c	4.808	SanAntonio	<Null>	0.143297	0.00045
10	Polygon	1629827	2135100	619	12c	0.557	SanAntonio	<Null>	0.042042	0.000052
11	Polygon	3585694	2139967	5274	12c	4.747	SanAntonio	<Null>	0.143301	0.000444
12	Polygon	1629511	2135049	5796	12c	5.216	SanAntonio	<Null>	0.12878	0.000488
13	Polygon	1628203	2135005	8400	12c	7.56	SanAntonio	<Null>	0.156497	0.000707
14	Polygon	3585762	2140001	143	12c	0.129	SanAntonio	<Null>	0.022643	0.000012

Record: 1 Show: All Selected Records (0 out of *2000 Selected) Options

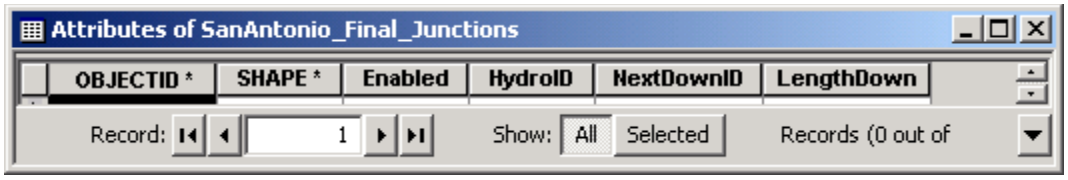
3. We will need to add the following fields to the three tables:

   a. For the junction featureclass, add the fields:

      i. HydroID (long integer)

      ii. NextDownID (long integer)

      iii. LengthDown (double)



   b. For the flowline featureclass, add the fields:

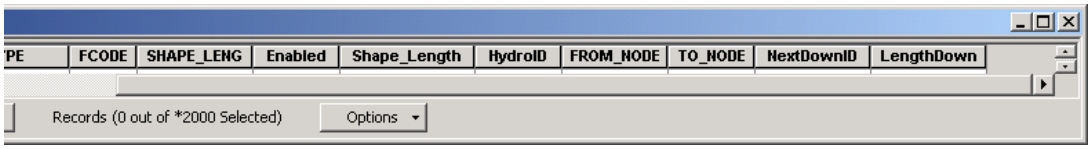
      i. HydroID (long integer)

      ii. From_node (long integer)

      iii. To_node (long integer)

      iv. NextDownID (long integer)

      v. LengthDown (double)



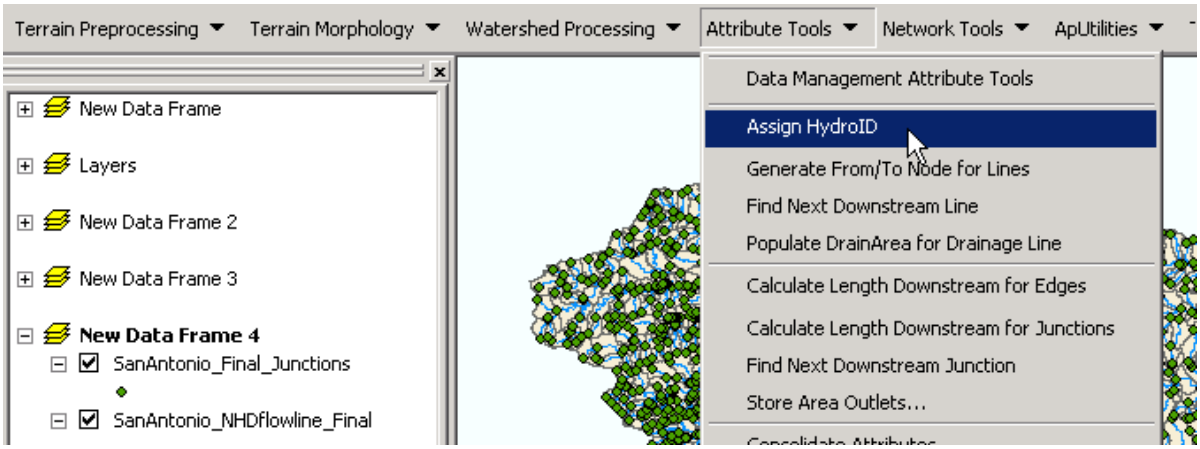
   c. For the flowline featureclass, add the fields:

      i. HydroID (long integer)

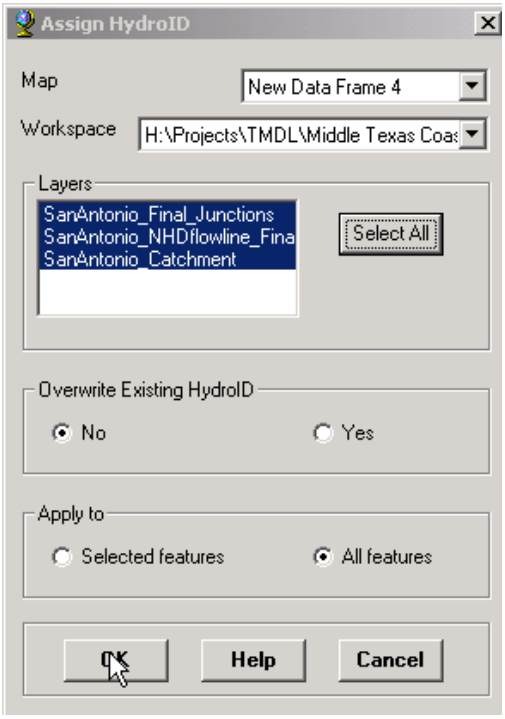
      ii. JunctionID (long integer)

Phase II: Populate fields

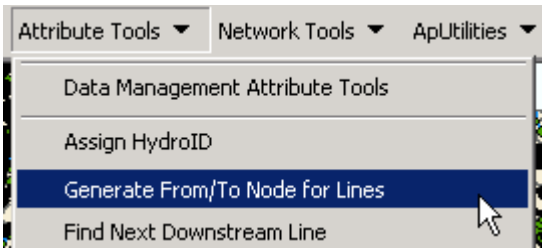
1. Arc Hydro uses unique HydroIDs to identify featureclasses in a geodatabase and establish their relationships. To assign HydroID, go to the Arc Hydro Toolbar, click on ***Attribute Tools*** and select ***Assign HydroID.***

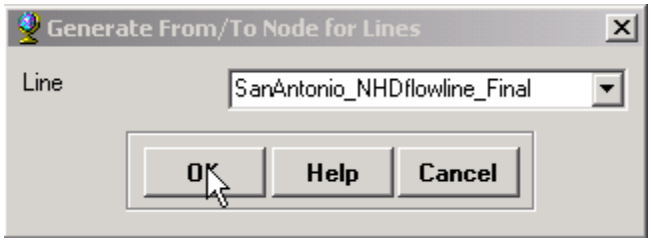


2. ***Select All*** layers in the data frame and hit **OK**.

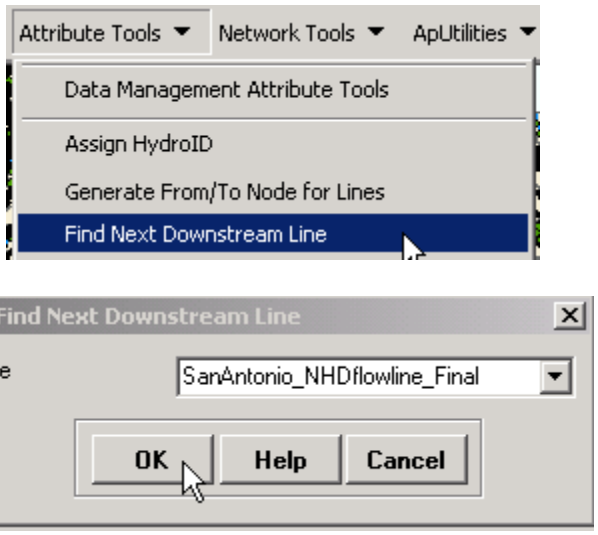


3. Next populate the FromNode and ToNode fields in the flowline featureclass as shown below.

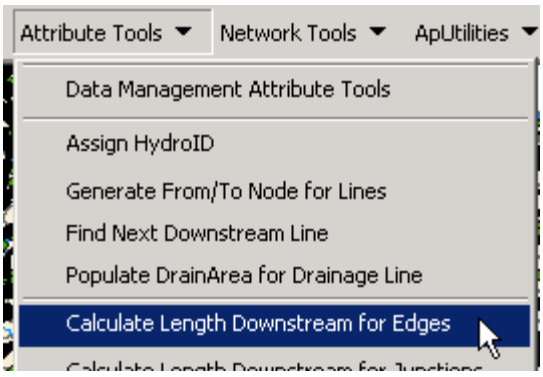




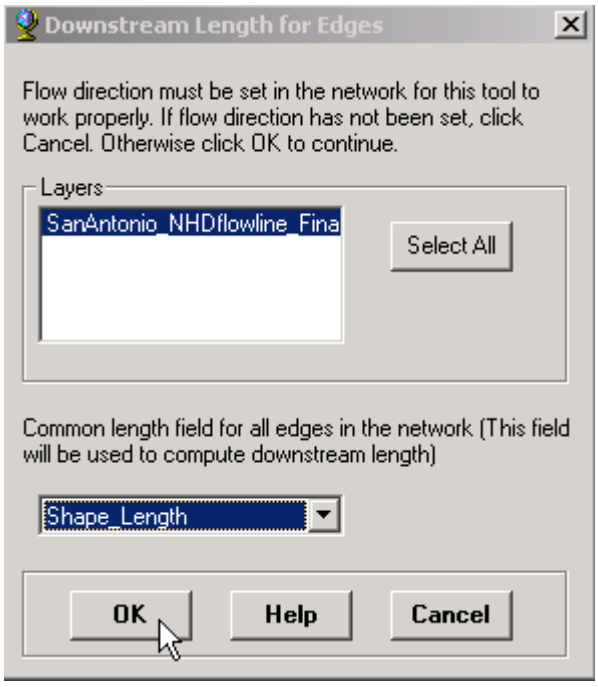
4. Next populate the NextDownID in the flowline feature class by going to ***Attribute Tools*** again and select ***Find Next Downstream Line*** as shown below.



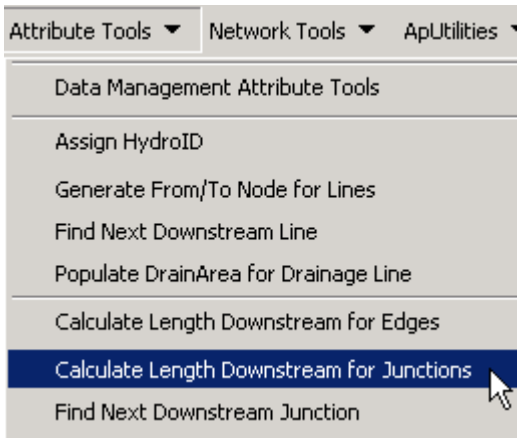
5. After that calculate the length downstream for the flowline featureclass (as shown). This will populate the ***LengthDown*** field for the flowline featureclass.



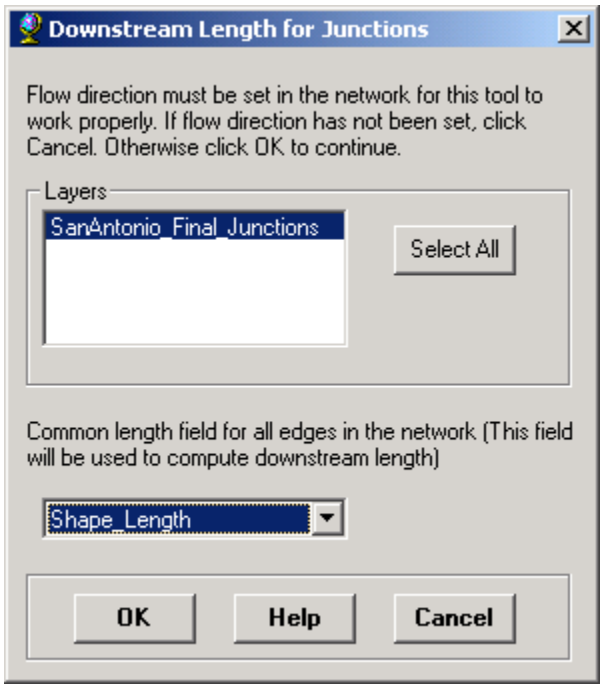
6. Specify the ***Shape_Length*** field as the length field as shown.



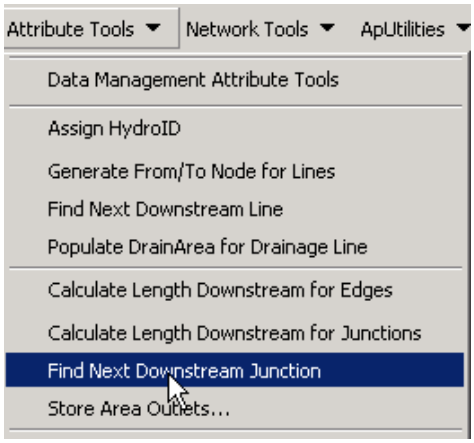
7. Next, calculate the length downstream for the junction featureclass as shown below. This will populate the ***LengthDown*** field for the junction featureclass.



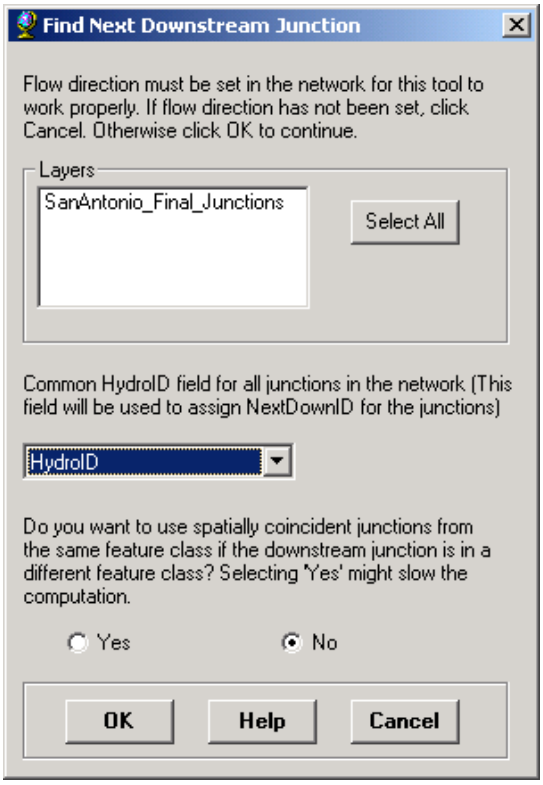
8. Specify the ***Shape_Length*** field as the length field as shown.



9. For each junction feature, we want to know which junction is immediately downstream of it based on the flow direction established in the flowline featureclass. Next go to the ***Arc Hydro Toolbar*** -> ***Find Next Downstream Junction.***



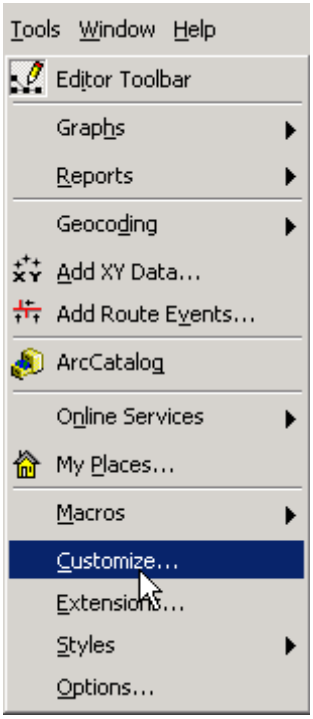
10. Click on ***SanAntonio_Final_Junctions***. Select ***HydroID*** as the common HydroID field for all junctions in the network and hit OK.



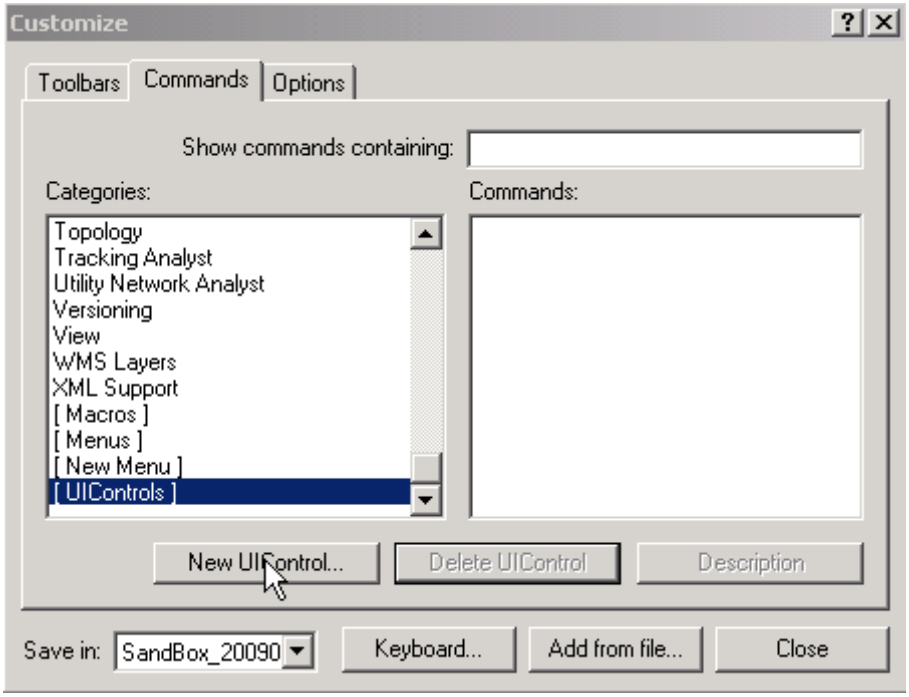
Phase III: Assign JunctionIDs to catchment featureclass

Finally let's find the junction that serves as the outlet of each catchment featureclass. Unfortunately, the ***Store Area Outlets*** function in Arc Hydro Tool does not work well with NHDPlus. Instead there is a workaround application written by Dr. Timothy Whiteaker at the University of Texas Center for Research in Water Resources (CRWR).

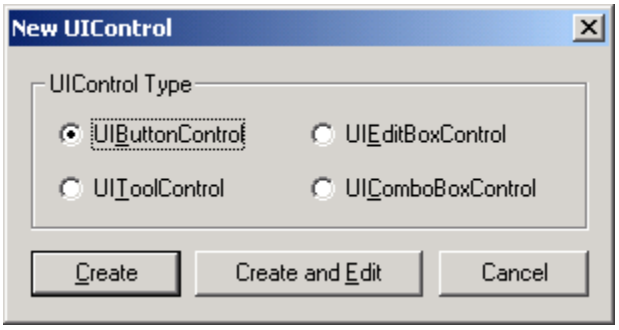
1. Let's add a button for this application to ArcMap. Right click on the main toolbar and scroll down to ***Customize***.

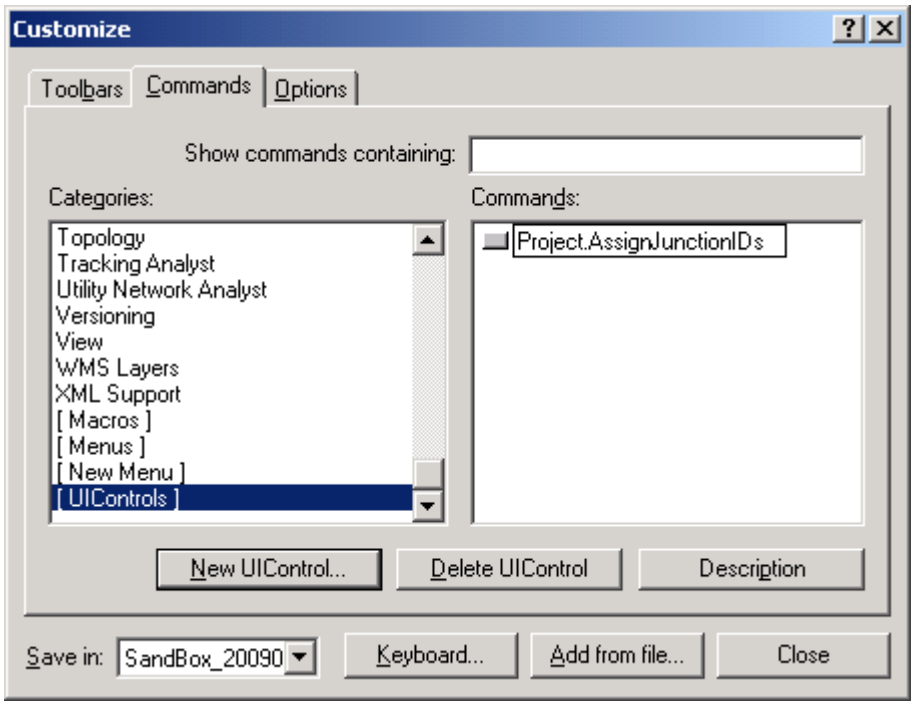


2. Click on the ***Commands*** tab and click on ***UIControls*** at the bottom of the left menu. Then click on ***New UIControl***.

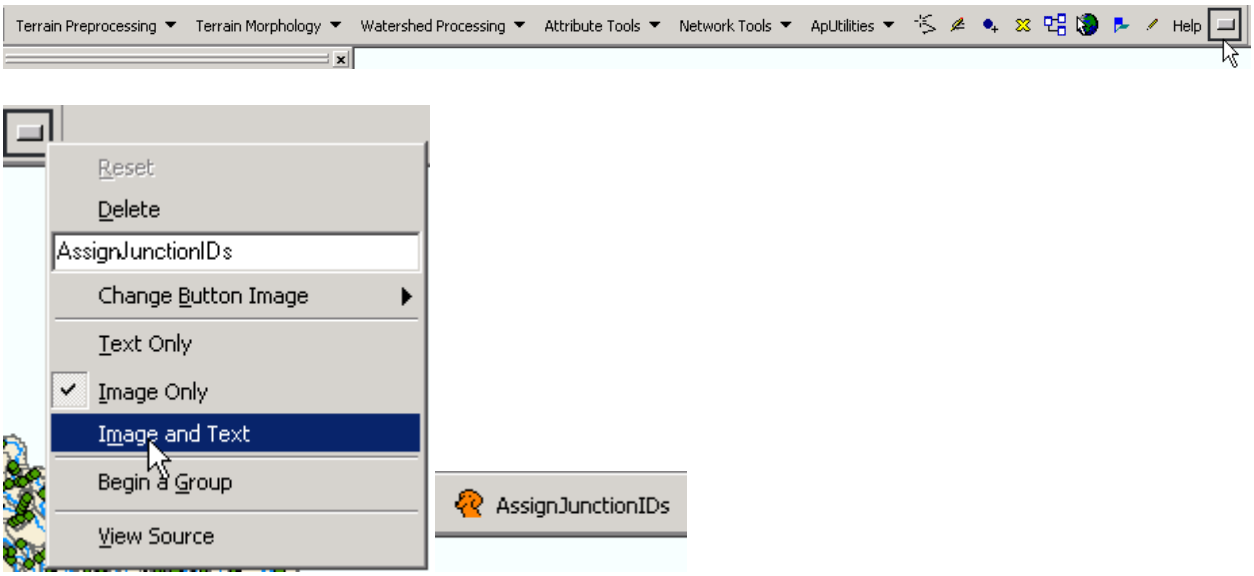


3. Select UIButtonControl and name the new button AssignJunctionIDs.

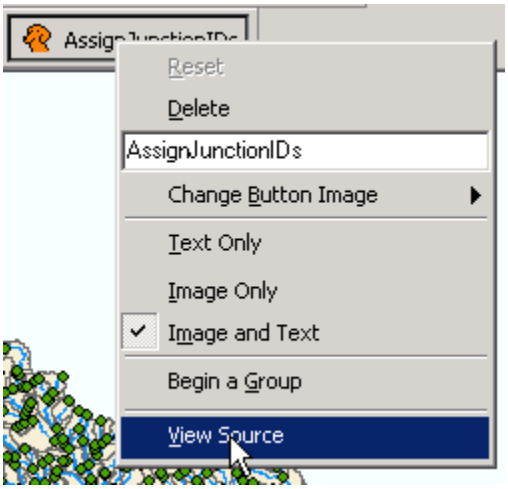




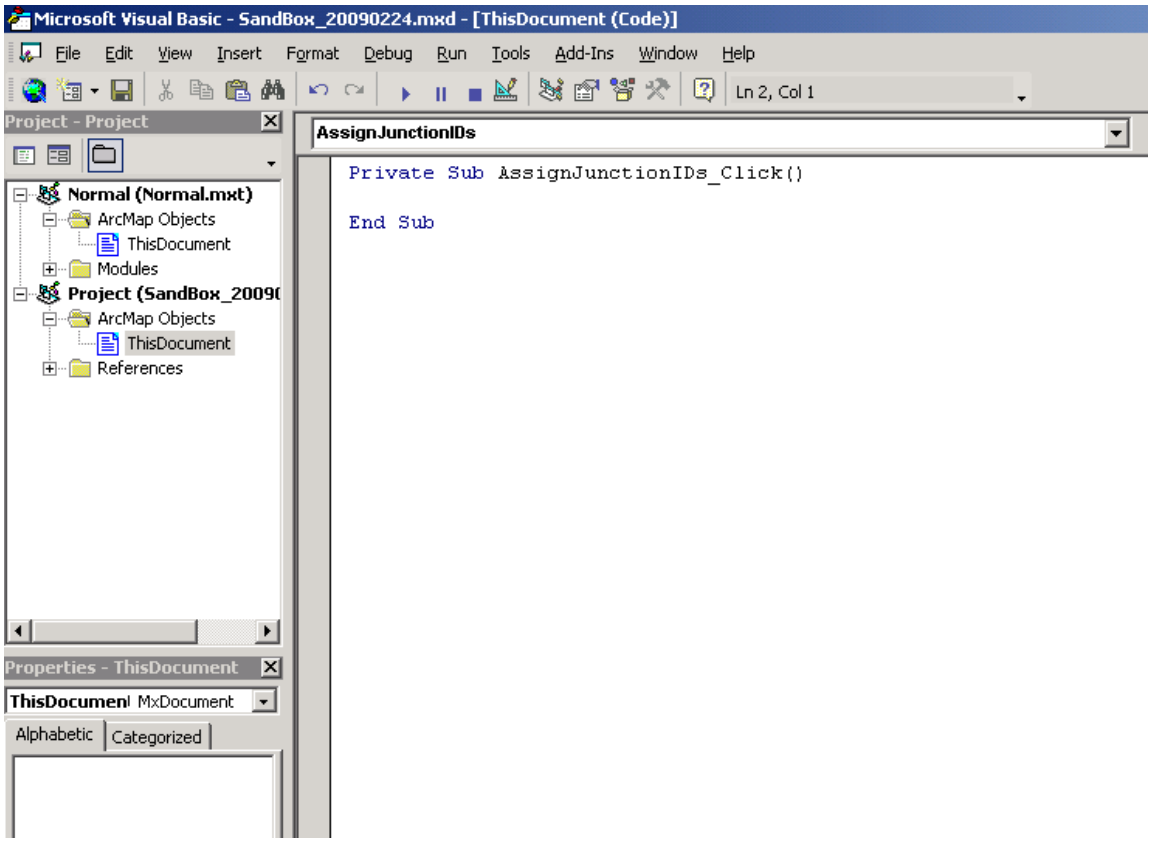
4. Drag this button to the edge of the Arc Hydro tool bar. **Do not close the Customize window.** Right click on the button and select ***Image and Text***. Feel free to change the button image as well.



5. Right click on the button and select view source.

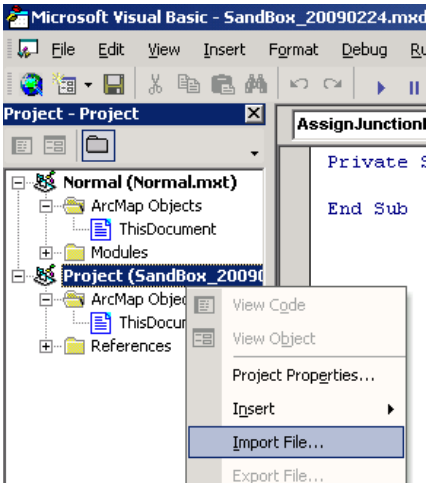


You will enter the Visual Basic editor screen.

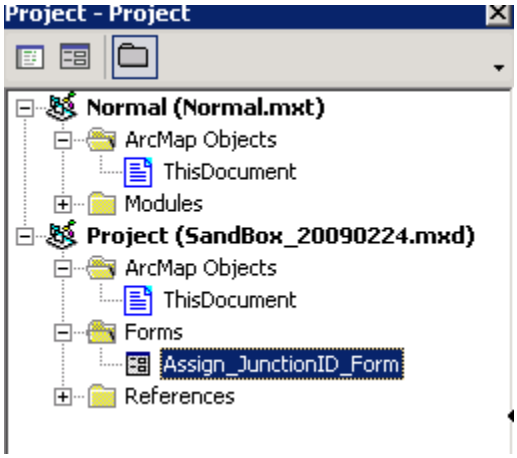


6. If you're working on this exercise at CRWR, you can find the programming code that you need on the network and can import it to your file. Right click on ***Project*** and select ***Import File…***. Import the form, ***Assign_JunctionID_Form.frm*** from the folder ***H:\Projects\TMDL\Middle Texas Coast\Models_for_waterbodies\Tools\Assigining_JunctionIDs.***

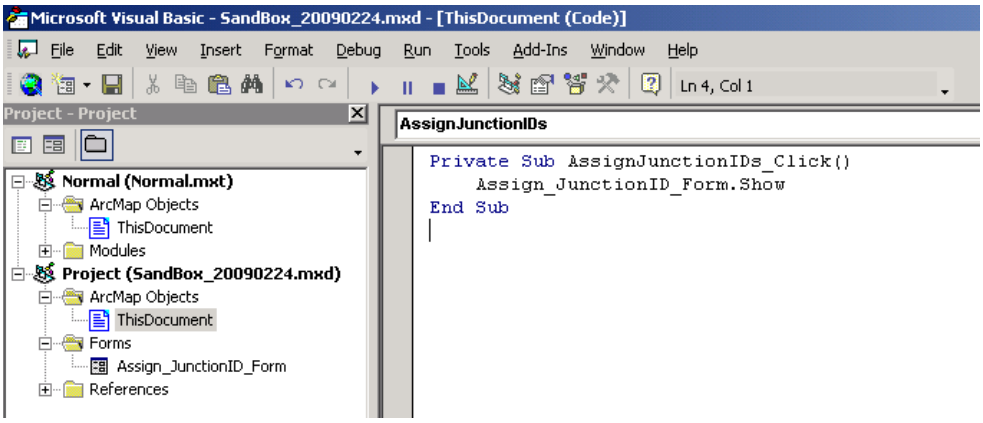
If you're not working at CRWR, you'll need to create your own user form before continuing. Skip down to the end of this tutorial for directions on how to create the necessary user form (see "General Information on the "Assign JunctionIDs" Form for use in Phase III"). Then return to this point, import your form, and continue the exercise.



The form will show up in the ***Form*** folder on the left panel.

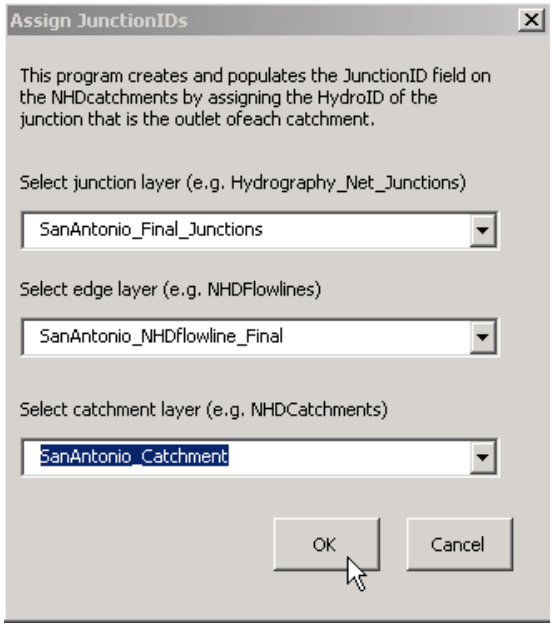


7. On the right panel, type in ***Assign_JunctionID_Form.Show*** in the ***AssignJunctionIDs_Click()*** subroutine. This will activate the form whenever the button is clicked.



8. Now close the visual basic editor and the ***customize*** window. Click on the ***AssignJunctionIDs*** button.

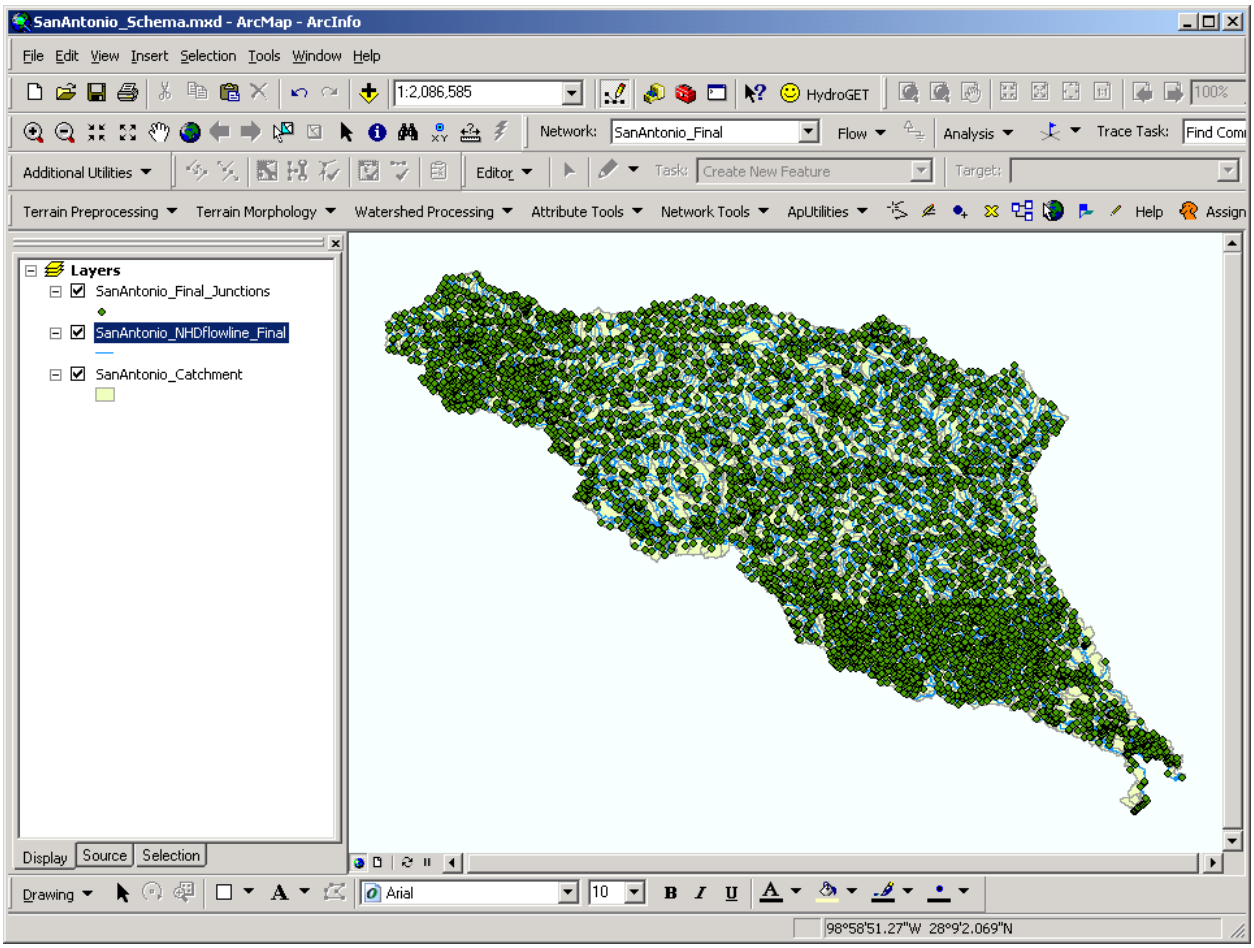
9. In the form, enter the layers to the processed as shown below. And then hit ***OK***. A message window will show up once the process is completed.



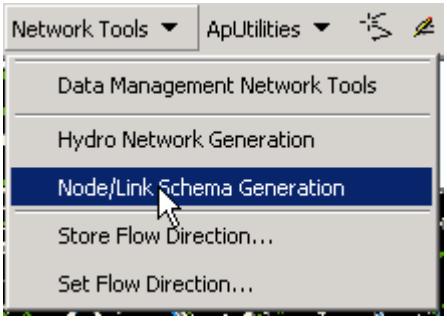
10. Once completed, save and close the project. We will create a new ArcMap project specifically to create the schema network.

Part IV: Generating the schematic network

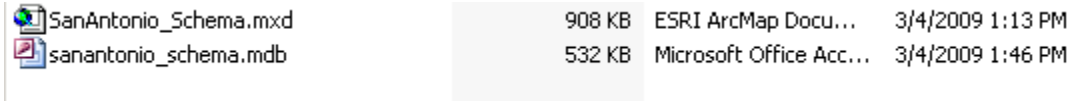
1. Create a new ArcMap project. Let's call it ***SanAntonio_Schema.mxd*** and open it up. Bring in the ***SanAntonio_Catchment*** and ***SanAntonio_Final*** network.



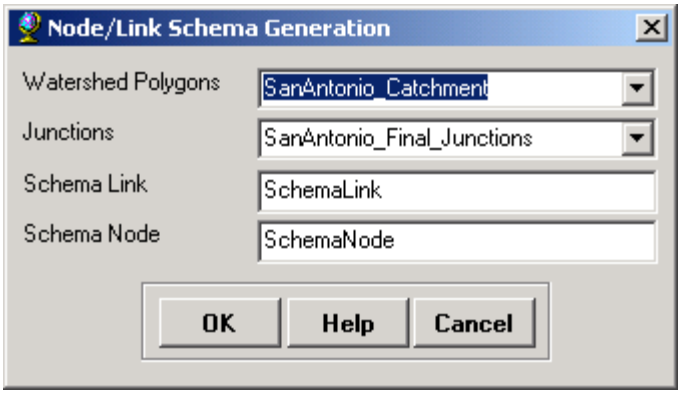
2. Within Arc Hydro tools, click on ***Network Tools*** and ***Node/Link Schema Generation***.



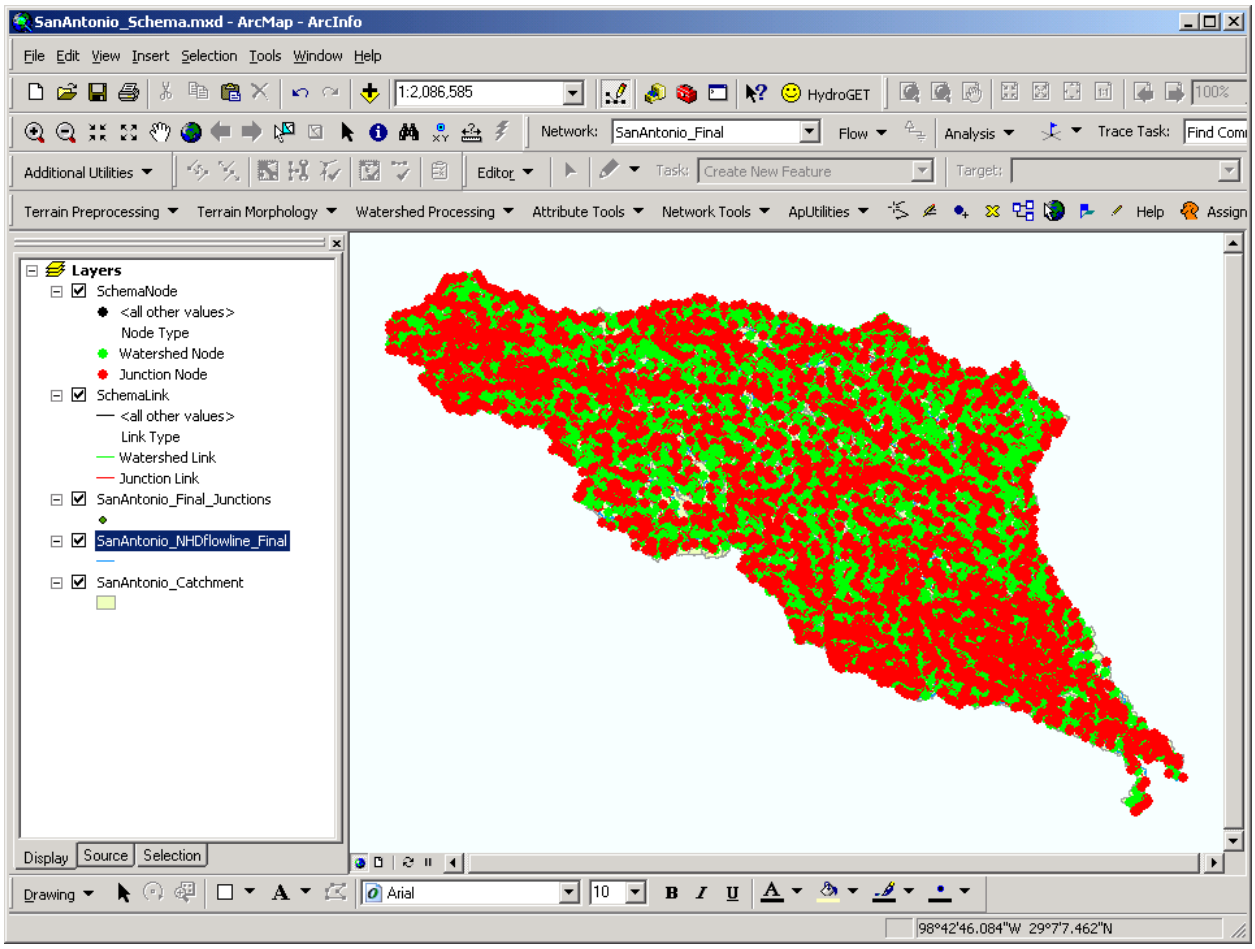
There will be a slight pause as Arc Hydro creates an empty geodatabase that has the same name as the project (in this case ***SanAntonio_Schema.mdb***) within the same directory.



3. The following dialog box will show up. Enter the input layers as shown then hit ***OK***.



This will take quite a while to complete (on the order of 30 minutes or so).

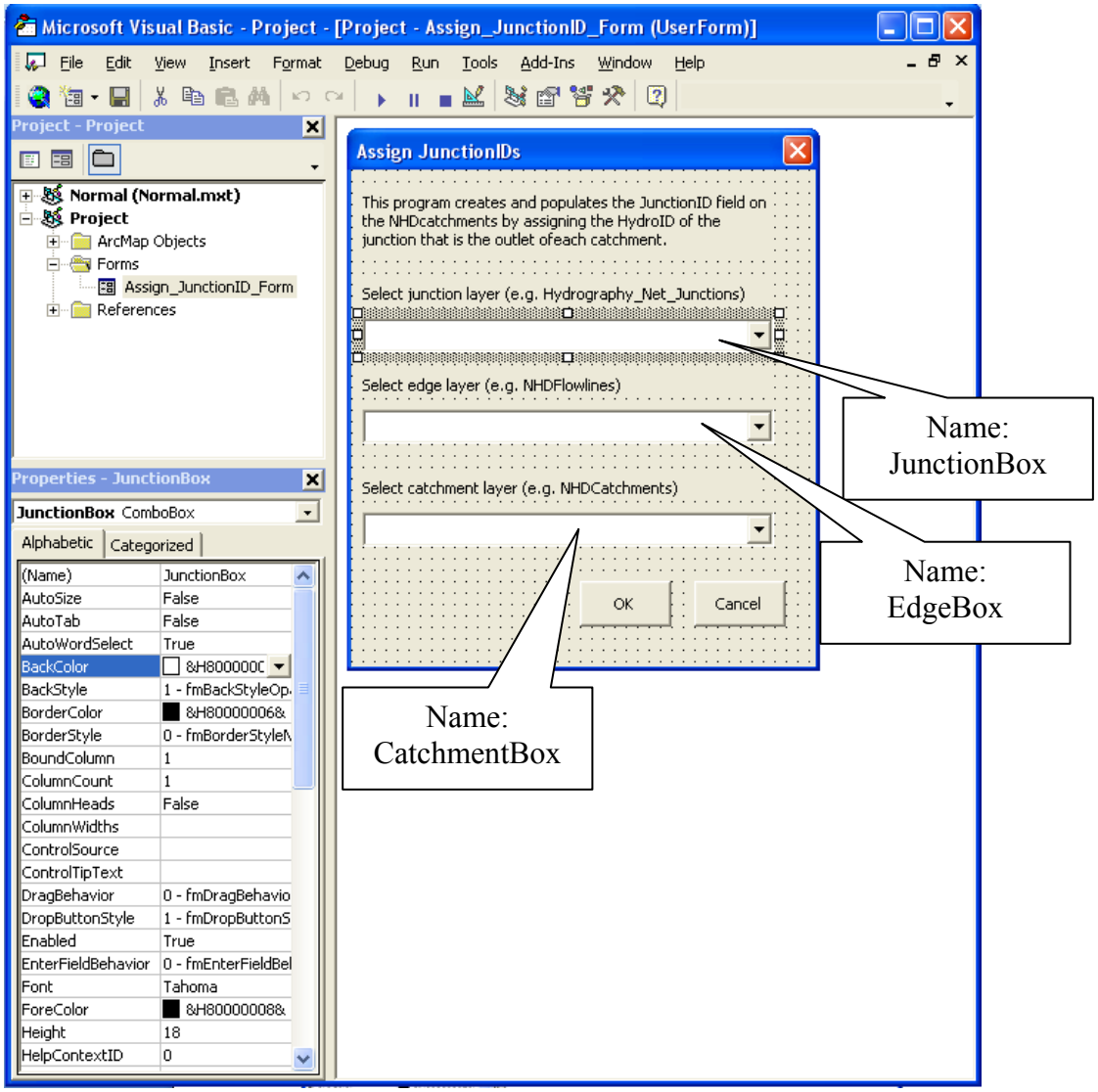


Congratulations, you have successfully generated a schematic network from NHDPlus!

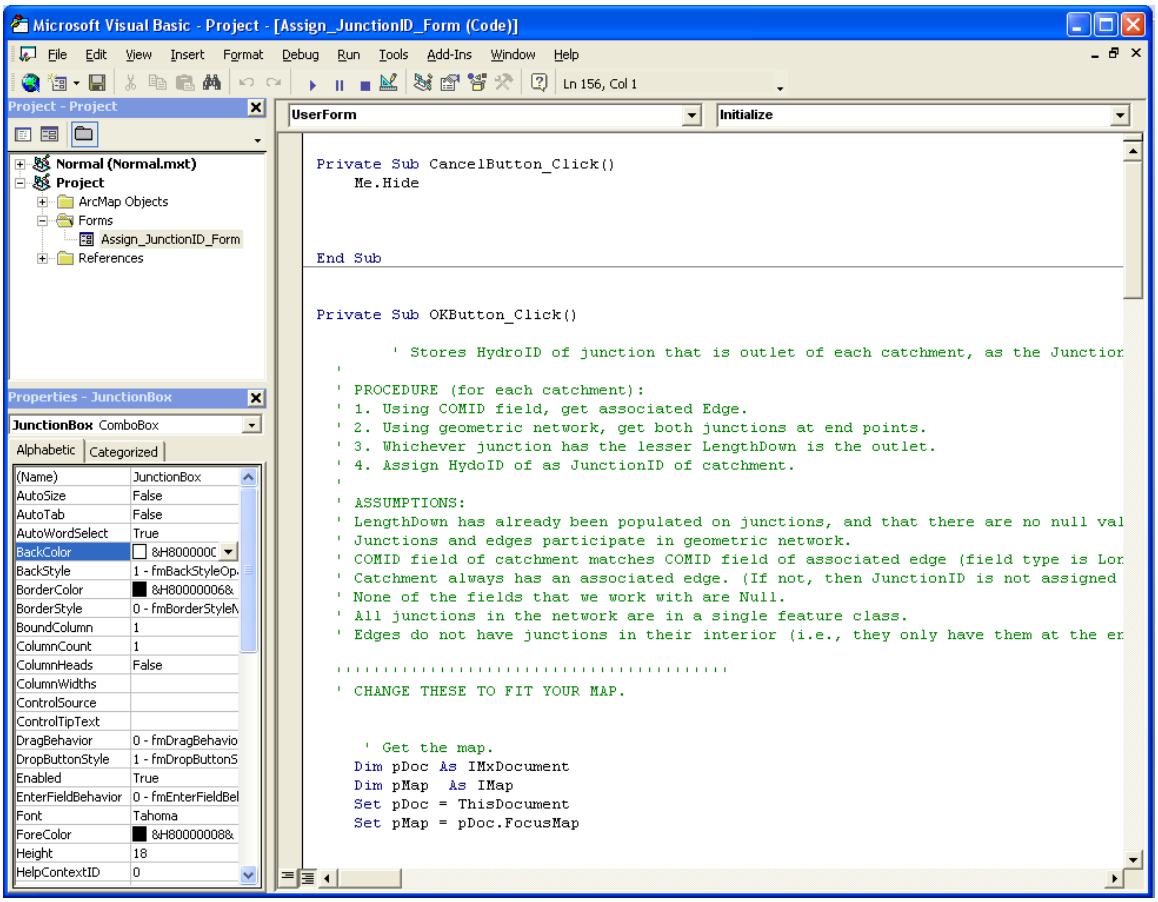
General Information on the "Assign JunctionIDs" Form for use in Phase III:

The following gives general information on creating the Assign JunctionIDs form that is discussed in Phase III, Step 8. If this form is not available, the user can re-create the form as shown below and continue with the Phase III procedure.

The user form should be designed as shown in the following screenshot, with the ComboBoxes being named: JunctionBox, EdgeBox, and CatchmentBox.



The programming code associated with the user form is shown below. The user can simply cut and paste the code into the Visual Basic Editor as shown in the figure.



Code:

```
Private Sub CancelButton_Click()
   Me.Hide

End Sub


Private Sub OKButton_Click()
```

```
    ' Stores HydroID of junction that is outlet of each catchment, as the JunctionID on the catchment.
 '
 ' PROCEDURE (for each catchment):
 ' 1. Using COMID field, get associated Edge.
 ' 2. Using geometric network, get both junctions at end points.
 ' 3. Whichever junction has the lesser LengthDown is the outlet.
 ' 4. Assign HydoID of as JunctionID of catchment.
 '
 ' ASSUMPTIONS:
 ' LengthDown has already been populated on junctions, and that there are no null values.
 ' Junctions and edges participate in geometric network.
 ' COMID field of catchment matches COMID field of associated edge (field type is Long).
 ' Catchment always has an associated edge. (If not, then JunctionID is not assigned to the catchment.)
 ' None of the fields that we work with are Null.
 ' All junctions in the network are in a single feature class.
 ' Edges do not have junctions in their interior (i.e., they only have them at the end points).

 """""""""""""""""""""""""""""""""""""""
 ' CHANGE THESE TO FIT YOUR MAP.

   ' Get the map.
   Dim pDoc As IMxDocument
   Dim pMap  As IMap
   Set pDoc = ThisDocument
   Set pMap = pDoc.FocusMap

   Dim player As IFeatureLayer
   Dim pfc As IFeatureClass

   Dim junctionLayerIndex As Long
   junctionLayerIndex = -999
   Dim edgeLayerIndex As Long
   edgeLayerIndex = -999
   Dim catchmentLayerIndex As Long
   catchmentLayerIndex = -999
```

```
  For i = 0 To pMap.LayerCount - 1
     If pMap.Layer(i).Name = JunctionBox.Text Then
        junctionLayerIndex = i
     End If
     If pMap.Layer(i).Name = EdgeBox.Text Then
        edgeLayerIndex = i
     End If
     If pMap.Layer(i).Name = CatchmentBox.Text Then
        catchmentLayerIndex = i
     End If
  Next i

  If junctionLayerIndex = -999 Then
     MsgBox ("You must choose a junction layer")
     Exit Sub
  End If

  If edgeLayerIndex = -999 Then
     MsgBox ("You must choose a edge layer")
     Exit Sub
  End If

  If catchmentLayerIndex = -999 Then
     MsgBox ("You must choose a catchment layer")
     Exit Sub
  End If

''''''''''''''''''''''''''''''''''''''''
 ' Get the layers and fields from the map.
Dim junctionLayer As IFeatureLayer
Dim junctionClass As IFeatureClass
Set junctionLayer = pMap.Layer(junctionLayerIndex)
Set junctionClass = junctionLayer.FeatureClass
Dim lengthDownFldIndex As Long
lengthDownFldIndex = junctionLayer.FeatureClass.Fields.FindField("LengthDown")
Dim hydroIdFldIndex As Long
hydroIdFldIndex = junctionLayer.FeatureClass.Fields.FindField("HydroID")

Dim edgeLayer As IFeatureLayer
Set edgeLayer = pMap.Layer(edgeLayerIndex)
Dim eComIdFldIndex As Long
eComIdFldIndex = edgeLayer.FeatureClass.Fields.FindField("COMID")
```

```
Dim catchmentLayer As IFeatureLayer
Set catchmentLayer = pMap.Layer(catchmentLayerIndex)
Dim cComIdFldIndex As Long
cComIdFldIndex = catchmentLayer.FeatureClass.Fields.FindField("COMID")
Dim junctionIdFldIndex As Long
junctionIdFldIndex = catchmentLayer.FeatureClass.Fields.FindField("JunctionID")

' Get a cursor pointing to our features to process.
Dim pQF As IQueryFilter
Set pQF = New QueryFilter
'pQF.WhereClause = "ObjectID = 425" ' For testing.
Dim catchmentCursor As IFeatureCursor
Set catchmentCursor = catchmentLayer.Search(pQF, False)
Dim catchment As IFeature
Set catchment = catchmentCursor.NextFeature

' Loop through all catchments.
Dim edgeCursor As IFeatureCursor
Dim edge As IEdgeFeature
Dim fromJunction As IFeature, toJunction As IFeature
Dim hydroID As Long

Do Until catchment Is Nothing
  ' Counter.

  i = i + 1
  Debug.Print i

  ' 1. Using COMID field, get associated Edge.
  pQF.WhereClause = "COMID = " & catchment.Value(cComIdFldIndex)
  Set edge = edgeLayer.Search(pQF, False).NextFeature

  If Not edge Is Nothing Then
    ' 2. Using geometric network, get both junctions at end points.
    Set fromJunction = edge.FromJunctionFeature ' This only returns a feature with an OID, Enabled, and Shape field.
    Set fromJunction = junctionClass.GetFeature(fromJunction.OID) ' Get a feature with all fields.
    Set toJunction = edge.ToJunctionFeature ' This only returns a feature with an OID, Enabled, and Shape field.
```

```
    Set toJunction = junctionClass.GetFeature(toJunction.OID) ' Get a feature with all
fields.

    ' 3. Whichever junction has the lesser LengthDown is the outlet.
    If                    fromJunction.Value(lengthDownFldIndex)                    >
toJunction.Value(lengthDownFldIndex) Then
      hydroID = toJunction.Value(hydroIdFldIndex)
    Else
      hydroID = fromJunction.Value(hydroIdFldIndex)
    End If

    ' 4. Assign HydoID of as JunctionID of catchment.
    catchment.Value(junctionIdFldIndex) = hydroID
    catchment.Store
  End If

  Set catchment = catchmentCursor.NextFeature
 Loop

 MsgBox "Finished"
 Me.Hide
End Sub


Private Sub UserForm_Initialize()
Dim pDoc As IMxDocument
  Dim pMap As IMap
  Dim player As IFeatureLayer

  'Get the current map
  Set pDoc = ThisDocument
  Set pMap = pDoc.FocusMap

  '  Looping through the contents of the TOC

  count_shapefile = 0
  For i = 0 To pMap.LayerCount - 1

    Dim player1 As ILayer
    Set player1 = pMap.Layer(i)

    If TypeOf player1 Is IFeatureLayer Then
```

```
        Set pfeaturelayer = pMap.Layer(i)

        Assign_JunctionID_Form.JunctionBox.AddItem (player1.Name)
        Assign_JunctionID_Form.EdgeBox.AddItem (player1.Name)
         Assign_JunctionID_Form.CatchmentBox.AddItem (player1.Name)

        count_shapefile = count_shapefile + 1
        End If

    Next i
        If count_shapefile = 0 Then
            MsgBox "Error:  Cannot find a single shapefile in the dataframe."
            Exit Sub
        End If
End Sub
```

Appendix B: Calculating Inputs to the TMDL Balance Model

Calculating Inputs to the TMDL Balance Model

By: Stephanie L. Johnson

INTRODUCTION

The purpose of this appendix is to provide further insight on the approaches used to compute inputs to the TMDL Balance model as used to compute fecal coliform loadings in the Copano Bay watershed under mean annual conditions (described in Chapters 4 and 5 of this dissertation). The first section of the appendix describes how nonpoint sources loadings were distributed across the watershed, focusing mainly on the quantification and distribution of agricultural animals and wildlife. Also included in this section is a summary of wastewater treatment plant loadings. The second portion of the appendix provides details on the methods used to calculate travel times associated with overland flow through the catchments and within the tidal river segments. The final section of the appendix supports the water and bacteria balance outlined in Chapter 5 by giving more details on computing the variables discussed in the dissertation text.

FECAL COLIFORM LOADINGS

Nonpoint Sources (Agricultural Animals, Wildlife, Septic Systems, and Land Use)

The fecal coliform loading from agricultural animals and wildlife are accounted for on a per unit basis. The measure of units, in this case, was the animal unit (AU). The AU is a common unit in agricultural science and is defined as 1000 pounds of animal.

For example, an adult beef cow is assumed to weigh approximately 1000 pounds and is, therefore, considered 1 AU. A deer, on the other hand, is much smaller and is considered to be 0.112 AUs. The number of agricultural and wildlife animals in the watershed, the corresponding AUs, and the expected load per AU are based on estimates from a 2009 Texas A&M AgriLife Extension report (Moench and Wagner, 2009). This report uses land use/land cover (LULC) data from the 2001 National Land Cover Dataset (NLCD) to estimate the number of animals in the Copano Bay watershed as a function of the number of animals in each county that makes up watershed and the percent of each county that lies in the watershed. For example, the report uses 2004-2008 agricultural census data to estimate that 23,400 beef cattle are present in Refugio County (Moench and Wagner, 2009). An analysis in ArcMap shows that 63% of Refugio County lies in the Copano Bay watershed, as shown in Figure B1. Based on this information, the report states that 14,674 of the beef cattle in Refugio County are in the Copano Bay watershed. A similar analysis is completed for the other counties in the watershed (Aransas, Bee, Goliad, Karnes, and San Patricio) to estimate an overall total of 66,348 beef cattle in the Copano Bay watershed. This exercise is performed for the remainder of the agricultural and wildlife animals, to estimate the number and fecal coliform loading of each bacterial source. Table B1 summarizes their findings for the entire watershed. For clarity and comparison purposes, the animal population numbers discussed in this appendix and dissertation will refer to number of animals (not AUs) from this point forward.

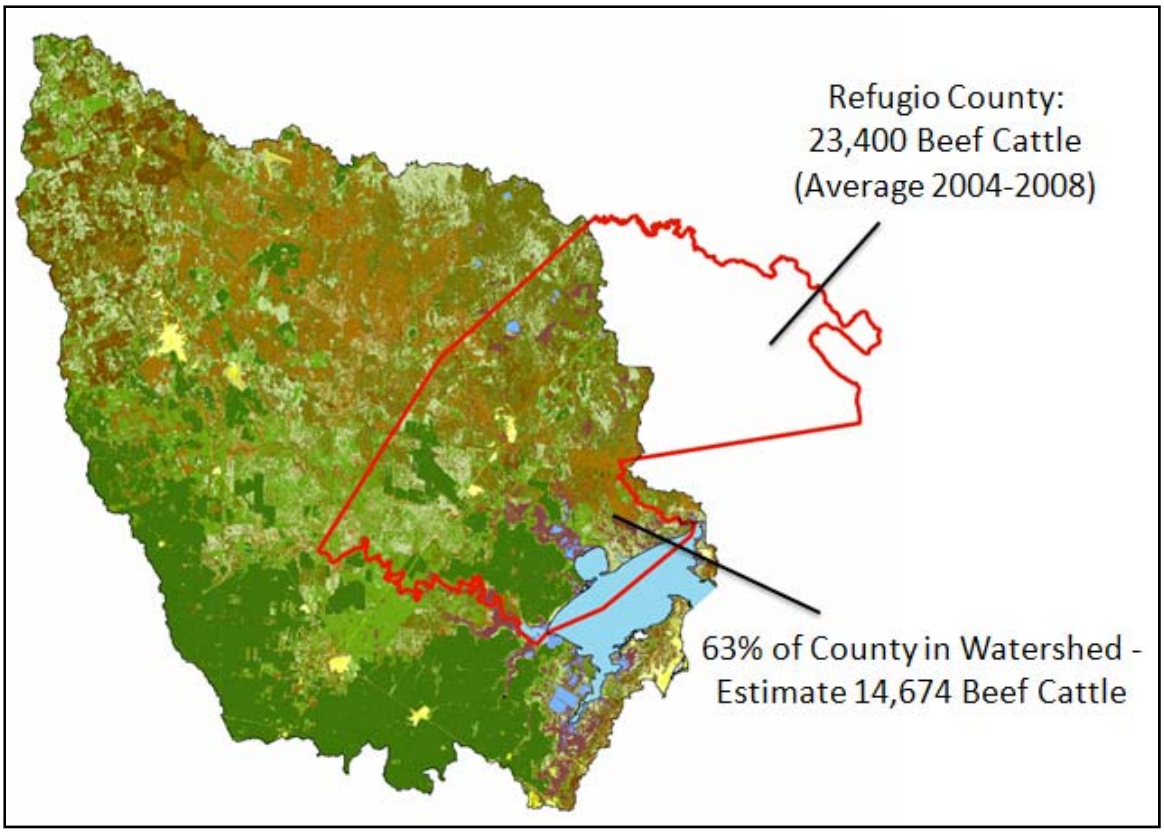


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Figure B1: Estimating the Number of Refugio County Beef Cattle in the Watershed

Table B1: Agricultural and Wildlife Animals in the Copano Bay Watershed (Moench and Wagner, 2009)

Animal	Number of Animals	Number of AUs	Fecal Coliform Loading (10^9 CFU/AU/day)	Fecal Coliform Loading (10^{15} CFU/yr)
Beef Cattle	66,348	66,348	8.55	207
Horses	2,479	3,100	0.291	0.33
Goats	3,611	615	25.4	5.70
Sheep	927	185	290	19.6
Hogs	623	156	97.3	5.54
Layers	1,377	13	37.1	0.19
Pullets	542	5	37.1	0.07
Broilers	673	7	48.4	0.12
Turkey	28	0	6.18	0.001
Deer	88,850	9,951	15.0	54.4
Feral Hogs	37,718	4,715	1.21	2.08

For use in the TMDL Balance model, the nonpoint sources have to be divided among the catchments of the Copano Bay watershed. To accomplish this task, the most likely LULC(s) for each nonpoint source to be located on were assessed. For example, Moench and Wagner (2009) indicate that beef cattle will be mainly present on six different LULC categories: deciduous forest, evergreen forest, mixed forest, shrub/scrubland, grasslands/herbaceous, and pasture/hay. Feral hogs, however, will be present on 8 different land use types: the 6 that cattle are on, plus cultivated crops, and woody wetlands (Moench and Wagner, 2009). The report uses these data to estimate an average stocking rate (in area/animal) for these land uses in the Copano Bay watershed. For this work, we combined the reported average stocking rates with the NLCD 1992 data to compute the nonpoint sources per catchment and the overall number in the

watershed. Though NLCD 2001 data were used in the AgriLife study and 1992 data are used in our analysis, the NLCD datasets are similar enough that the difference in the resulting total animal numbers in the watershed is minimal. However, in cases of minor discrepancies, the stocking rates were slightly adjusted until the total number of animals per watershed matched that presented by Moench and Wagner (2009). When distributing the animals across the watershed, all agricultural animals were assigned to the same LULC types as beef cattle. However, while the cattle stocking rates fluctuated per LULC type (Moench and Wagner, 2009), stocking rates for the other animals are assumed constant across LULC types. Deer were assigned to the same LULC types as feral hogs, again with a constant stocking rate.

Figure B2 shows an example of the distribution and fecal coliform loading calculation for catchment 5297607 (i.e., the catchment with COMID 5297607). The LULC within this catchment is classified as shown in Table B2, with the primary land use being shrubland. Stocking rates were applied to the catchment to reveal the animal populations shown in Figure B2 (e.g., this catchment contains 630 beef cattle, 643 deer, and 20 horses). Failing septic systems (or on-site sewage facilities [OSSFs]) were assigned to LULC Types 21 and 22 (low and high intensity residential); details on computing the number of failing OSSFs are given in Appendix C. Since these land uses are not present in this catchment, no failing OSSFs were assigned to it. Finally, the LULC Types 21, 22, 23, 61, 82, 83, 85, 91, and 92 were considered to contribute bacterial loading from overland runoff. The area of these LULCs in the catchment was noted and EMCs were applied based on literature values and previous studies in the area (Gibson, 2006; USEPA 2001; Zoun, 2003). Loadings due to overland runoff from the

other land uses were accounted for through the bacterial loadings from the animals that were assigned to those areas.

Table B2: Land Use in Catchment 5297607

NLCD 1992 Code	Land Use/Cover Description	Percent Coverage
NLCD_11	Open Water	0
NLCD_12	Perennial Ice/Snow	0
NLCD_21	Low Intensity Residential	0
NLCD_22	High Intensity Residential	0
NLCD_23	Commercial/Industrial/Transportation	0.38
NLCD_31	Bare Rock/Sand/Clay	0.17
NLCD_32	Quarries/Strip Mines/Gravel Pits	0.04
NLCD_33	Transitional	0
NLCD_41	Deciduous Forest	9.92
NLCD_42	Evergreen Forest	7.11
NLCD_43	Mixed Forest	0
NLCD_51	Shrubland	27.09
NLCD_61	Orchards/Vineyards/Other	0
NLCD_71	Grasslands/Herbaceous	12.88
NLCD_81	Pasture/Hay	24.68
NLCD_82	Row Crops	17.49
NLCD_83	Small Grains	0.04
NLCD_84	Fallow	0
NLCD_85	Urban/Recreational Grasses	0
NLCD_91	Woody Wetlands	0.01
NLCD_92	Emergent Herbaceous	0.19

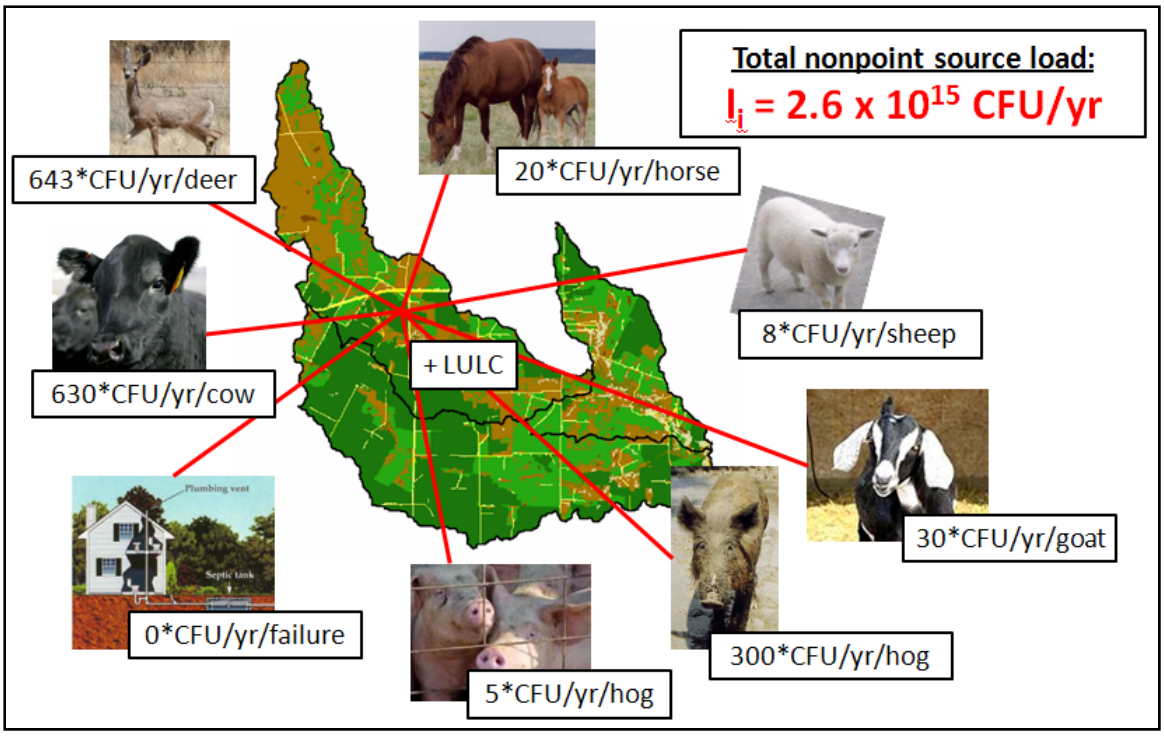


Figure B2: Computing Fecal Coliform Loading from Catchment 5297607

The fecal coliform load from each nonpoint source in catchment 5297607 is summarized in Table B3. The resultant total nonpoint source load (2.64×10^{15} CFU/m^3) was then entered into TMDL Balance model as the mean annual fecal coliform load associated with the Type 1 SchemaNode that represents this catchment. The same process was repeated for the other 640 Type 1 SchemaNodes in the watershed. Results of the overall analysis are discussed in Chapter 4.

Table B3: Load from Various Sources in Catchment 5297607

Source	Number of Animals/OSSFs	Load (10^{15} CFU/year)
Beef Cattle	630	1.97
Horses	20	0.00274
Goats	30	0.0476
Sheep	8	0.164
Domestic Hogs	5	0.0466
Poultry	12	0.00284
Deer	643	0.0166
Feral Hogs	300	0.395
LULC	----	0.00000000017
Failing Septic Systems	0	0
Total		***2.64***

Wastewater Treatment Plants

WWTP loadings are modeled as the product of the expected mean concentration (EMC) of fecal coliform in each effluent and the reported mean annual flow from each plant. The mean annual flow is used for this calculation per request of staff at the Texas Commission on Environmental Quality (TCEQ). This was requested because, in practice, the plants are never allowed to meet their maximum permitted flow. Table B4 lists the reported average discharge and modeled EMCs of fecal coliform from each plant. EMC values are computed as the average of all samples collected from the plant effluent during the intensive sampling discussed in Chapter 3. The last column of the table shows the mean annual load that was modeled from each WWTP.

Table B4: WWTP Permitted and Reported Flows

Permit Number	Permittee	EMC of Fecal Coliform (CFU/100mL)	Reported Avg Discharge (m^3/year)	Modeled Mean Fecal Coliform Loading (10^{12} CFU/year)
10055-001	City of Sinton	287	766,515	2.20
10124-002	City of Beeville	9	3,025,605	0.27
10124-004	City of Beeville	1	573,831	0.01
10156-001	Town of Woodsboro	13	159,454	0.02
10237-001	City of Odem	793	186,494	1.48
10255-001	Town of Refugio	6,931	424,951	29.54
10705-001	City of Taft	3,868	600,498	23.22
10748-001	Pettus MUD	1	94,532	0.001
13412-001	TX Dept of Transportation	1	109	0.0
13641-001	City of Sinton	3,000	1,468	0.04
13892-001	Town of Bayside	56	38,133	0.02
14112-001	Skidmore Water Supply Corporation	1	34,185	0.0003
14119-001	St Paul Water Supply Corporation	1,144	43,063	0.49
14123-001	Tynan Water Supply Corporation	58,198	12,574	7.32
Total			***5,961,411***	***64.61***

COMPUTING TRAVEL TIMES

Overland Runoff

The total travel time from a nonpoint bacterial source in the watershed to Copano Bay (or a tidal river segment) consists of the time to travel through the catchment via overland flow plus the time to move downstream through the river system. As discussed in Chapter 4 of the dissertation, travel times within the non-tidal river segments are modeled according to the modeled streamflow and velocity calculations using the Jobson (1996) method. However, information on travel times within the catchments is not available. For the purposes of this work, the Soil Conservation Service (SCS) lag time method is used to estimate the travel time of overland flow within each catchment. It is then assumed that the travel time of the bacterial loading from the catchment is the same as the time of travel of the water (since bacterial contamination is assumed to move with the water).

The SCS lag time (T_{lag}) is an empirical approach to computing the travel time of overland flow based on physical data from a watershed (Mays, 2001). Equation B1 shows this empirical equation, where lag time is defined as the time from the centroid of excess rainfall on a watershed (defined as the rainfall in excess of infiltration capacity, evaporation, transpiration, and other losses) to the peak of the hydrograph resulting from that precipitation, as shown in Figure B3. Lag time is computed as a function of the LULC within the watershed (expressed through the curve number [CN]), the length of the longest drainage path in the watershed, and the average slope of the watershed.

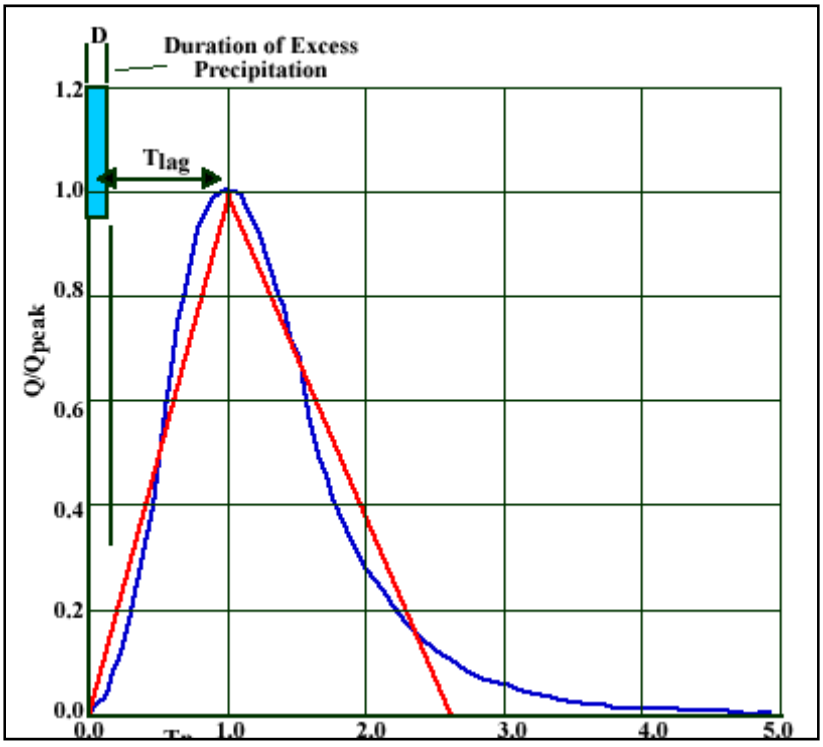
$$T_{lag} = \frac{L^{0.8} * (S+1)^{0.7}}{1900 * (\%slope)^{0.5}} \quad \text{(B1)}$$

Where: T_{lag} = lag time of overland flow (hours)

L = length of the longest drainage path (feet)

S = (1000/CN) - 10

%slope = average watershed slope (%)



Source:

http://www.juniata.edu/projects/nwsuhgmodule/content/topic3_synthetic/scs_page2.htm

Figure B3: SCS Lag Time

A CN is an estimate of the runoff potential from a given LULC; the larger the CN, the higher the runoff potential. For example, the CN of an impervious area (such as a parking lot) is 98 (NRCS, 1986). The CN of straight row crops under poor soil conditions on Hydrologic Type A soils is 72; with poor conditions on Hydrologic Type D Soils it is 91; and with good soil conditions on Hydrologic Type D soils it is 89 (NRCS, 1986). Therefore, when considering CNs on some of the LULC categories, the condition and hydrologic classification of the soil type are important. (Hydrologic soil groups indicate the type of soil being described. Type A soils are sand, loamy sand, and/or sandy loam, while Type D indicates clay based soils.) All CNs presented in this work assume type II antecedent soil moisture conditions.

Weighted curve numbers were computed for each catchment as shown in Table B5, using catchment 5297607 as an example. NLCD 1992 LULC data (from the NHDPlus "CatchmentAttributesNLCD" value added attribute [VAA] table) is used to determine the area of each LULC category in each catchment. Curve numbers were then assigned to each LULC type based on hydrologic soil type D (the most dominant soil type in the watershed) (Soil Survey Staff, 2008a) and fair hydrologic conditions, as shown in Table B5. Weighted curve numbers were computed for each catchment as a function of the area of each LULC category in that catchment and the assumed CN per category. The weighted CN for catchment 5297607, for example, is modeled as 82.

Table B5: Computing the Weighted Curve Number for Catchment COMID 5297607

NLCD 1992 Code	Land Use/Cover Description	Percent Coverage	Assumed Curve Number for LULC category
NLCD_11	Open Water	0	0
NLCD_12	Perennial Ice/Snow	0	98
NLCD_21	Low Intensity Residential	0	84
NLCD_22	High Intensity Residential	0	87
NLCD_23	Commercial/Industrial/Transportation	0.38	98
NLCD_31	Bare Rock/Sand/Clay	0.17	89
NLCD_32	Quarries/Strip Mines/Gravel Pits	0.04	89
NLCD_33	Transitional	0	---
NLCD_41	Deciduous Forest	9.92	79
NLCD_42	Evergreen Forest	7.11	79
NLCD_43	Mixed Forest	0	79
NLCD_51	Shrubland	27.09	79
NLCD_61	Orchards/Vineyards/Other	0	85
NLCD_71	Grasslands/Herbaceous	12.88	78
NLCD_81	Pasture/Hay	24.68	84
NLCD_82	Row Crops	17.49	89
NLCD_83	Small Grains	0.04	87
NLCD_84	Fallow	0	83
NLCD_85	Urban/Recreational Grasses	0	84
NLCD_91	Woody Wetlands	0.01	0
NLCD_92	Emergent Herbaceous	0.19	0

Figure B4 shows the estimated CNs for all the catchments in the watershed showing larger values in the southern portion of the watershed where agricultural land use is more prevalent (note in Table B5 that row crops, for example, have a high CN). Results give a weighted average CN of 78 for the entire watershed.

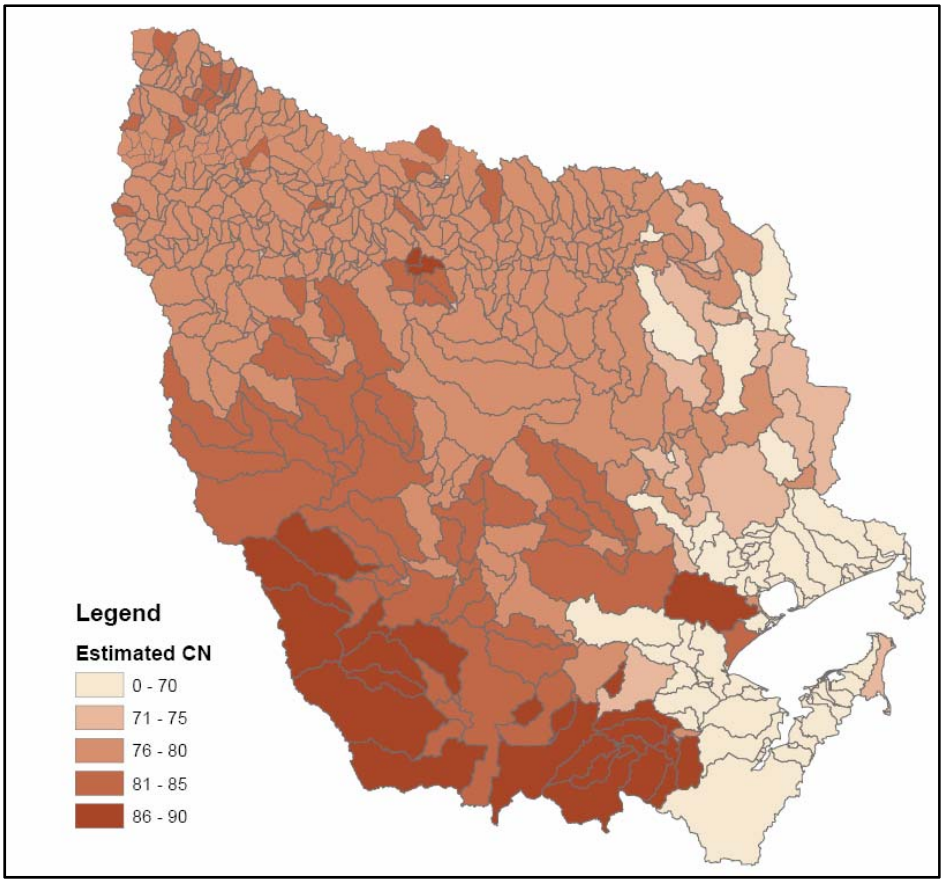


Figure B4: Estimated CNs for the Copano Bay Watershed

The Arc Hydro Terrain Preprocessing tools were used to compute the longest flow path and average % slope in each catchment of the watershed from the data contained in the NHDPlus flow direction grid and digital elevation model (DEM), respectively. Figure B5 shows the results of using the "Longest Flow Path for Catchments" tool to compute flow lengths in the catchments. Figure B6 shows the results of using the "Slope" tool to compute average slopes (as percents). The longest

flow path for catchment 5297607 is modeled as 64,555 ft; the average catchment slope is computed as 1.68%.

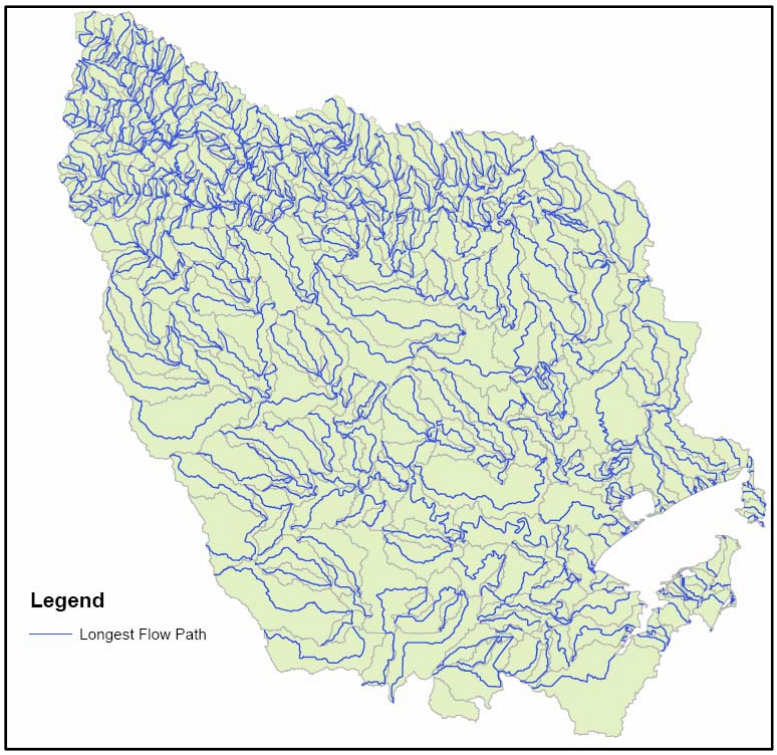


Figure B5: Longest Flow Path in the Catchments of the Copano Bay Watershed

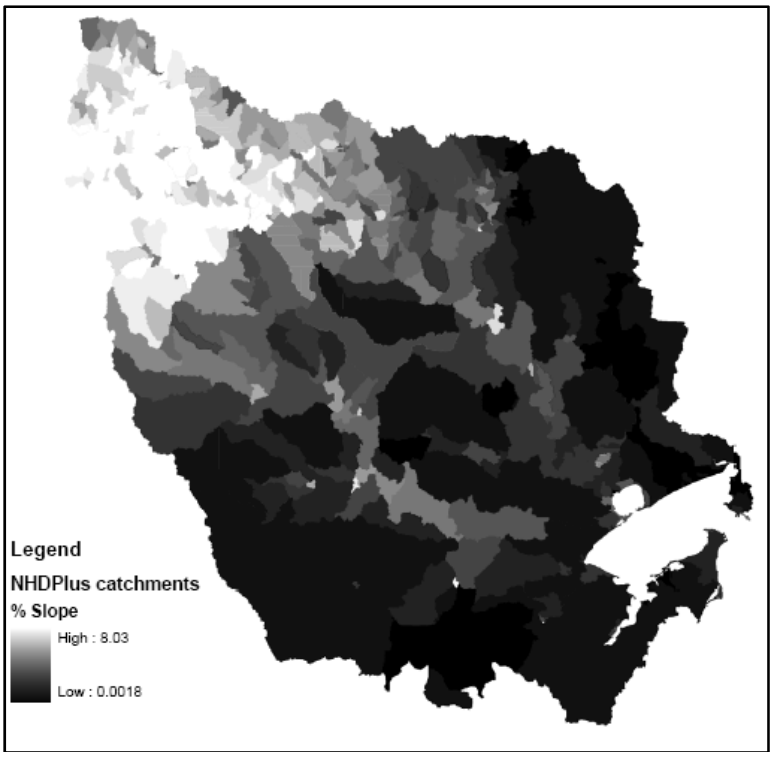


Figure B6: Average Percent Slope per Catchment in the Copano Bay Watershed

Results of these analyses were combined with the estimated CNs in the SCS lag time equation (Equation B1) to compute the lag time for each catchment in the watershed. The lag time for catchment 5297607 is computed to be 6.49 hours. The resultant lag times are assumed to equal the travel time of bacteria via overland flow through the catchments and were assigned to the appropriate SchemaLinks (Type 1) in the TMDL Balance model.

Tidal River Segments

One of the challenges of modeling water quality in coastal watersheds is the difference in the hydraulics of non-tidal and tidal river segments. Tidal river segments have the potential to experience much longer hydraulic residence times than do non-tidal rivers due to tidal impacts and backwater effects. However, up to this time, the flow in the tidal river sections of the Mission and Aransas Rivers were considered only under non-tidal (i.e., purely riverine) conditions. NHDPlus, for example, estimates velocities in these segments using the Jobson method, which treats the segments as non-tidal in nature. Previous modeling in the watershed (Gibson, 2006) also considered these segments under purely riverine flow. Ignoring the tidal impacts in these segments could cause considerable error in computing the loading to Copano Bay and Mission and Aransas Tidal Rivers. Therefore, in this work, we account for tidal hydraulics when modeling these river segments. Ideally, the tidal river segments would have been modeled using the tidal prism approach (as was used for Copano Bay and is discussed in Chapter 5). However, sufficient data are not available to characterize the tidal interactions between the tidal rivers and Copano Bay. Therefore, the tidal rivers are modeled as completely stirred tank reactors (CSTRs), which accounted for a portion of the impact of tidal hydraulics on the rivers.

Recent work at The University of Texas Marine Science Institute (UTMSI) shows that the Mission and Aransas Tidal River segments operate more like a bay than a river under all but the highest flow conditions. Under normal flow, the tidal rivers experience a portion of water that "sloshes" back and forth between the river segment and the Copano Bay. Then, under periodic high flow conditions, the system flushes itself out.

Such a flushing event occurred in the Aransas River in late July, 2008 (Mooney, 2008) when water quality sampling showed the movement of nitrogen through the system and the flushing of saline water. Monitoring after the storm showed the hydrology returning to normal conditions and the salinity values gradually rebounded to normal levels (Mooney, 2008).

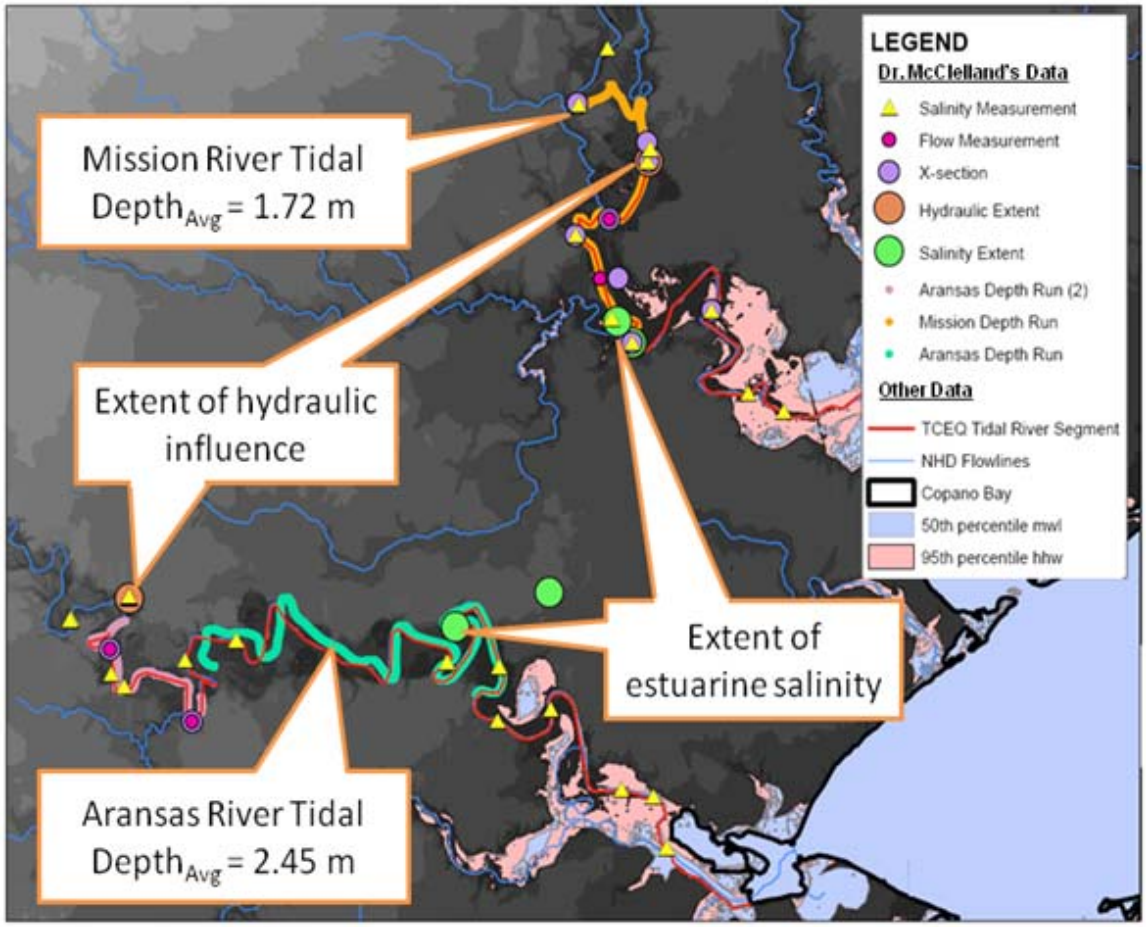


Figure B7: Results of McClelland Field Work on Mission/Aransas Tidal River Segments

To gain insight to the physical attributes of the Mission and Aransas Tidal Rivers, the UTMSI team performed a number of research cruises during the Summer of 2008. Figure B7 shows the tidal segments of the Mission and Aransas Rivers as defined by the TCEQ (for the purposes of water quality regulation) and the extent of salinity and hydraulic influences as measured by McClelland's team during their June and July 2008 fieldwork. Also shown are the paths that McClelland's team followed during these cruises, while taking continuous depth measurements of the center of the streams and the average depths that were measured during those runs. Approximately 5,000 depth measurements were taken during these cruises, revealing an average depth (d_1) of approximately 2.45 meters in the Aransas River and 1.72 meters in the Mission River. Cross-sectional measurements show that the rivers maintain a fairly flat elevation for the center ½ of the cross-section and then slope up to the river bank. The data collected are not detailed enough to perform a thorough calculation of the tidal rivers' bathymetry, but they give sufficient information to approximate the shape of the tidal river segments. Based on the data collected, the generic cross-section in Figure B8 is used to approximate the tidal segment volumes.

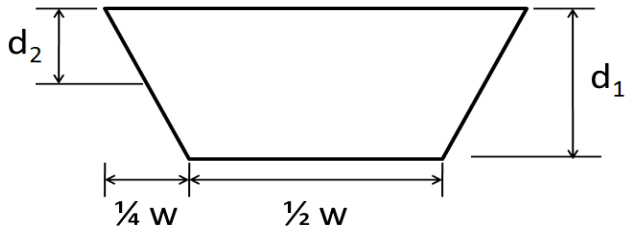


Figure B8: Generic Cross-Section of Mission and Aransas Tidal River Segments

Where: d_1 = average depth of the river segment (m)

d_2 = average depth of river at 1/8 of river width (m); data show $d_2 \approx 0.65 * d_1$

w = representative width of the river segment (m)

Tidal river volumes were computed based on the average tidal river depths, widths, and lengths shown in Table B6. Representative widths of the tidal river segments were estimated from aerial photography contained in Google Earth (accessed in August 2008). The length of the tidal river section was computed as defined by the TCEQ (see Figure B7). Equation B2 was used to compute the total volume of each segment.

Table B6: Physical Attributes of Mission and Aransas Tidal River Segments

	Aransas River	**Mission River**	**Source of Data**
Length (m)	44,302	27,664	NHDPlus
Representative Width (m)	54	41	Google Earth - Aerial Photo
Average depth (d_1) (m)	2.45	1.72	UTMSI
Volume (m^3)	4.9×10^8	1.6×10^8	Calculated

$$V = L * d_2 * w \qquad \text{(B2)}$$

Where: V =volume of tidal river segment (m^3)

L = length of tidal river segment (m)

The tidal river volumes presented in Table B6 are used to approximate the hydraulic residence times in each segment, as shown in Equation B3. Note that the flow used in Equation B3 is the freshwater flow since sufficient data are not available to account for the Copano Bay water that will also be exiting the river on the ebb flow (see the discussion on the tidal prism method in Chapter 5 for more information on this concept). Also, the residence time calculations were all performed using the average tidal river volume, since more detailed information on volumes under fluctuating hydrologic conditions is not available.

$$T = V/Q \qquad \text{(B3)}$$

Where: T = freshwater residence time of tidal river segment (years)

V =volume of tidal river segment (m^3)

Q = volume of freshwater entering the tidal river segment from upstream flow and overland runoff (m^3/year)

Table B7 shows the residence time of the tidal river segments under a variety of flow conditions. Flow probabilities were computed by considering the historic records of discharge at the nearest US Geological Survey (USGS) gauging station at a given probability of flow and translating that flow to the outlet of the tidal river segment into Copano Bay using the Drainage-Area Ratio Method. Flows exiting the Aransas Tidal River are based on flows at USGS Station 08189700; flows exiting the Mission Tidal River are based on flows at USGS Station 08189500.

Table B7: Modeled Flows and Residence Times through the Tidal River Segments

Flow Conditions at Nearest USGS Gauging Station	Aransas River Tidal		Mission River Tidal	
	Modeled Flow at Outlet (cfs)	Modeled Residence Time (days)	Modeled Flow at Outlet (cfs)	Modeled Residence Time (days)
5th percentile	7	280	4	163
Median Annual	38	52	30	22
Mean Annual	261	8	325	2
95th percentile	411	5	725	0.9

Results show the dynamic nature of the hydrology in the watershed with residence times ranging from less than one day to months. Using this approach, the mean annual residence time of the tidal river segments is on the order of two to eight days (for comparison, NHDPlus estimates these residence times as one to two days). Therefore, accounting for tidal hydraulics in these segments is quite impactful on the load that is modeled to Copano Bay, since bacteria have a significantly longer time to decay.

WATER AND BACTERIA BALANCE ON COPANO BAY

Freshwater Flow from the Watershed

The mean annual volume of water running off of the watershed into Copano Bay is calculated based on land use/land cover information in the NLCD and regional regression equations previously developed at the Center for Research in Water Resources (CRWR) (Quenzer and Maidment, 1998; U.S. Geological Survey, 2007b; 2008). The analysis was completed using NLCD data from 1992 and 2001. Results show that the predicted mean annual flows resulting from the use of the 1992 dataset are more accurate

when compared to actual data at the USGS gauging stations throughout the watershed. This might be due to the fact that the regression equations were developed from data collected through the mid-1990s. A comparison of the NLCD 1992 and 2001 coverages per catchment show that NLCD 2001 classifies much more land as agricultural and urban than they did in the 1992 analysis. These LULC categories have a much higher runoff potential per area in the regression equations, leading to an over-prediction of runoff from the watershed. NLCD 1992 data are used for this work.

The NLCD 1992 contains 21 LULC categories as listed in Table B6. NHDPlus contains these data in the VAA table "CatchmentAttributesNLCD", where the percent of each land use type is recorded per catchment. According to these data, seventeen of the NLCD 1992 categories appear in the Copano Bay watershed. Figure B9 shows these data. The regional regression equations require the NLCD categories to be grouped into four general land use categories, as shown in Table B6. The runoff from each land use category was calculated according to the regional regression equations (Quenzer and Maidment, 1998).

Table B6: NLCD 1992 LULC Categories and Associated Grouping for Use in Regional Regression Equations

NLCD 1992 Code	Land Use/Cover Description	Category for Use in Regional Regression Equations
NLCD_61	Orchards/Vineyards/Other	Agriculture
NLCD_81	Pasture/Hay	
NLCD_82	Row Crops	
NLCD_83	Small Grains	
NLCD_31	Bare Rock/Sand/Clay	Rangeland, Forest, Barren, Other
NLCD_32	Quarries/Strip Mines/Gravel Pits	
NLCD_41	Deciduous Forest	
NLCD_42	Evergreen Forest	
NLCD_43	Mixed Forest	
NLCD_51	Shrubland	
NLCD_71	Grasslands/Herbaceous	
NLCD_91	Woody Wetlands	
NLCD_92	Emergent Herbaceous	
NLCD_21	Low Intensity Residential	Urban Land
NLCD_22	High Intensity Residential	
NLCD_23	Commercial/Industrial/Transportation	
NLCD_85	Urban/Recreational Grasses	
NLCD_11	Open Water	Water
NLCD_12	Perennial Ice/Snow	N/A
NLCD_33	Transitional	
NLCD_84	Fallow	

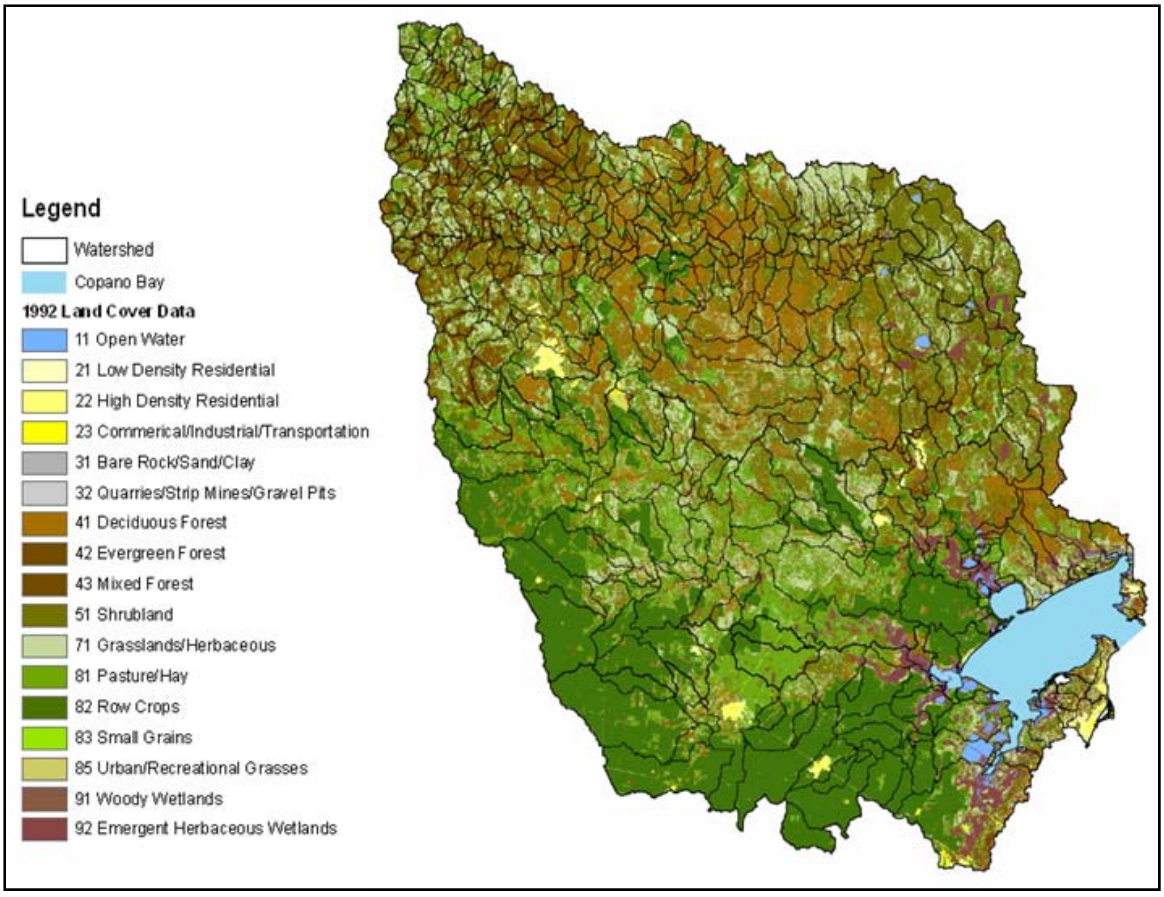


Figure B9: NLCD 1992 LULC in the Copano Bay Watershed

The total runoff per catchment was calculated as a function of the runoff from each LULC type and the percent the catchment covered in that LULC type.

$$q_j = [(f_{a,j} * q_{a,j} + f_{r,j} * q_{r,j} + f_{u,j} * q_{u,j} + f_{w,j} * q_{w,j}) * A_j] \quad \text{(B4)}$$

Where: q_j = Mean annual runoff from catchment j (m^3/year)

$q_{a,j}$ = Mean annual runoff from agricultural land in catchment j (m^3/m^2/year)

$q_{r,j}$ = Mean annual runoff from rangeland, etc. in catchment j (m^3/m^2/year)

$q_{u,j}$ = Mean annual runoff from urban land in catchment j (m^3/m^2/year)

$q_{w,j}$ = Mean annual runoff from open water in catchment j (m^3/m^2/year)

$f_{a,j}$ = Fraction of catchment j classified as agricultural land

$f_{r,j}$ = Fraction of catchment j classified as rangeland, etc.

$f_{u,j}$ = Fraction of catchment j classified as urban land

$f_{w,j}$ = Fraction of catchment j classified as open water

A_j = Area of catchment j (m^2)

In addition to overland flow, there are fifteen WWTPs that also contribute freshwater to Copano Bay. Table B4 lists the plants with their reported and permitted mean annual flows. As mentioned above, WWTP discharges are accounted for based on the plants' reported mean flows. The total amount of freshwater entering Copano Bay from the watershed is then the sum of the runoff from the catchments plus the discharge from the WWTPs in the watershed.

$$Q_f = \sum_{j=1}^{J} q_j + \sum_{i=1}^{I} q_i \quad \text{(B5)}$$

Where: q_i = Permitted mean annual discharge from WWTP i (m^3/year)

For this work, the total mean overland flow from the watershed to Copano Bay is computed as 6.31×10^8 m^3/year. The mean annual discharge from WWTPs is computed as 6.0×10^6 m^3/year. Therefore, the freshwater flow to Copano Bay is 6.37×10^8 m^3/year.

Physical Attributes of Copano Bay

The mean annual surface area and volume of Copano Bay were estimated using LiDAR data from the Texas Natural Resources Information System (TNRIS) (TNRIS, 2008), bathymetry data from previous reports (Ward, 1997), and water level data from the Texas Coastal Oceanic Observation Network (TCOON) station in Copano Bay (Texas A&M University - Corpus Christi, 2007; TNRIS, 2008; Ward, 1997). The TCOON data were analyzed over the complete period of record (1993-2007) to reveal an overall average water level of 0.19 m NAVD88. The LiDAR and bathymetry data were then used in the GIS-based Analytical Framework for Coastal and Estuarine Study (ACES) tool (Hampson and Bourne, 2007) to create Copano Bay's water surface and volume at an elevation of 0.19 m NAVD88. As a result, the mean annual surface area of Copano Bay is determined to be 2.12×10^8 m^2. The mean annual volume of the bay is calculated at 3.84×10^8 m^3.

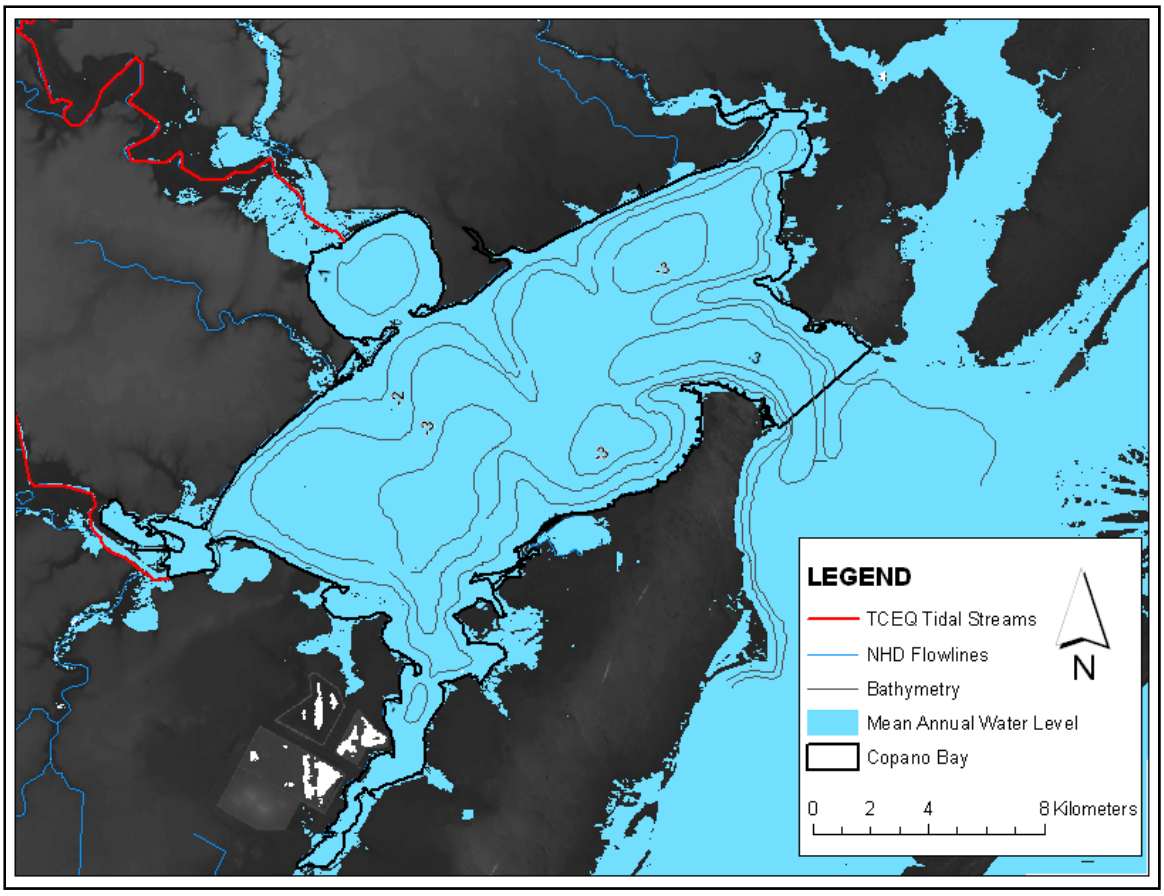


Figure B4: Mean Annual Surface Area of Copano Bay

Water Entering Bay from Precipitation

The amount of water entering Copano Bay through precipitation was calculated from the NHDPlus VAA table "CatchmentAttributesTempPrecip", which presents a mean annual precipitation for each catchment. The source of this information is the PRISM model from Oregon State University (2008). To determine the mean annual precipitation into Copano Bay, the mean annual precipitation in the catchments

immediately adjacent to the Bay was calculated through weighted averaging (weighted by area).

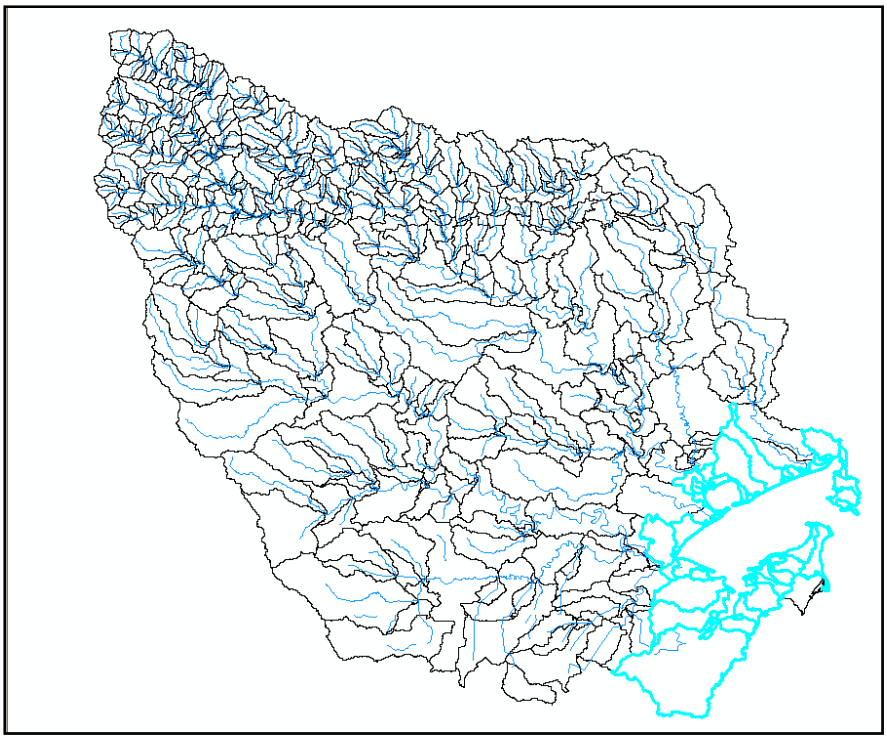


Figure B5: Computing the Mean Annual Precipitation onto Copano Bay

The mean annual precipitation (m/year) was then multiplied by the mean annual surface area of Copano Bay to obtain the mean annual amount of water entering Copano Bay through precipitation.

$$Q_p = P * SA \quad \text{(B6)}$$

Where: Q_p = Mean annual volume of precipitation entering Copano Bay (m^3/year)

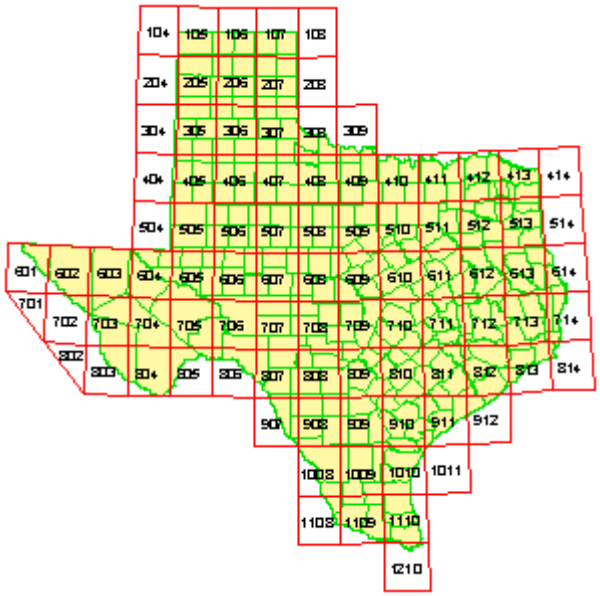
P = Mean annual precipitation in catchments immediately surrounding Copano Bay (m/year)

SA = Mean annual surface area of Copano Bay (m^2)

Using this approach, the mean amount of precipitation entering the bay is 0.891 m/year. Combining this with the mean annual surface are of the bay, the mean annual volume of water entering Copano Bay from precipitation is $1.88x10^8$ m^3/year.

Water Exiting Bay from Evaporation

The volume of water exiting Copano Bay due to evaporation was calculated from estimates of open water evaporation rates provided by the Texas Water Development Board (TWDB). The board separates Texas into quadrangles as shown in Figure B6. Copano Bay lies in quadrangle 910, which has a mean annual evaporation rate of 55.4 in/yr (1.35 m/yr) (calculated for the years 1954-2004).



Source: http://midgewater.twdb.state.tx.us/Evaporation/evap.html

Figure B6: TWDB Data Quadrangles

The mean annual evaporation rate was combined with the surface area of the Bay to calculate a mean annual amount of evaporation from Copano Bay of 2.86×10^8 m^3/year.

$$Q_e = E * SA \quad \text{(B7)}$$

Where: Q_e = Mean annual amount of evaporation exiting the Bay (m^3/year)

E = Mean annual rate of evaporation in Copano Bay area (m/year)

SA = Mean annual surface area of Copano Bay (m^2)

Appendix C: Estimating Failures of and Loadings from On-site Sewage Facilities in the Copano Bay Watershed

Estimating Failures of and Loadings from On-site Sewage Facilities in the Copano Bay Watershed

By: Stephanie L. Johnson

Many of the households in the study area use on-site sewage facilities (OSSFs) as their primary mode of septic disposal. Malfunctioning OSSFs are known to be a potential cause of bacterial contamination in both surface and groundwaters. However, the likelihood and amount of contamination attributable to OSSFs is not an easily quantified figure, due both to the complexity of the systems involved and to the unseen nature of the system's functionality. In this appendix we estimate the amount of bacterial contamination due to OSSFs in the Copano Bay watershed by using state, local, and federal data on the number of OSSFs in the watershed. Literature data on the likelihood of septic system failure were combined with information on areal soils and depth to groundwater to estimate the number of failing OSSFs. Finally, literature values were used to estimate the amount of bacteria moving from those failing OSSFs into the surface waters of our study area.

BACKGROUND

OSSF Functionality

A conventional OSSF consists of two components: a septic tank and a drain field (see Figure C1). Septic tanks are designed to provide the necessary residence time

(typically 6 to 24 hours) to remove settleable and floatable materials and anaerobically digest the retained organic matter. Pathogens and nutrients are not effectively removed in a conventional system, so significant concentrations of these pollutants are released in the effluent. Drain fields are relied upon to provide conditions supportive of further treatment of the septic effluent through biological processes, adsorption, filtration, and infiltration. The condition of the soil surrounding the drain field of a conventional system is, therefore, very important in avoiding pathogen and nutrient contamination.

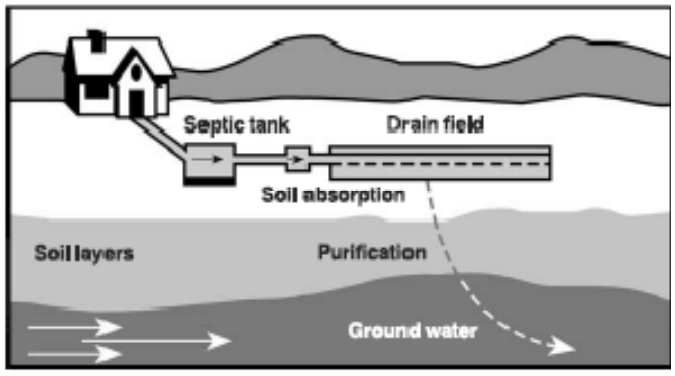


Figure reproduced from: USEPA, 2002.

Figure C1: Conventional On-site Wastewater Treatment System

In terms of removing bacteria from the septic effluent, the soil underlying the drain field can be thought of in three zones: the infiltration zone, the vadose zone, and the saturated zone. The infiltration and vadose zones combine to act as a fixed-film bioreactor, performing the majority of the physical, chemical, and biological treatment that the septic effluent will undergo. If the soil is adequate for use in a drain field, a

sufficient biomat is formed (usually in the first few centimeters of the infiltration zone) and enough oxygen is present, >99.99% of fecal coliform is generally removed in the first 3 to 5 feet of strata (USEPA, 2002).

Unfortunately, only about 1/3 of the soils in the United States are considered suitable for use in conventional drain fields (USEPA, 2002). Typical characteristics of an unsuitable soil would be those that are subject to frequent flooding, those with a high groundwater table, or those in a tight geological formation (e.g., clay). Such soils either do not provide an adequate vertical distance for treatment in the infiltration and vadose zones or do not provide aerobic conditions. In these cases, bacterial contamination of the shallow groundwater aquifer is commonly found.

OSSFs can also fail based on the operations within the septic tank itself. Such failure is normally the result of a hydraulic overload of the tank, reducing the residence time to the point where effective treatment cannot occur. Causes of a low residence time may be a septic tank that was too small to begin with, a household using more water than the tank was designed for, or a reduction of the tank's effective volume through poor maintenance and a build-up of sludge. Since the septic tank does not remove a significant portion of the bacteria to begin with, in this work we were more concerned with failure due to inadequate drain field conditions.

OSSF Failure

The definition of OSSF failure is not universal. One definition might be where the system is overloaded to the point of water ponding on top of the ground, while

another mightconsider less obvious symptoms such as inadequate depth to the groundwater table. A number of methods are available for estimating the percent of OSSF failures in the Copano Bay watershed. One option is to review the Texas Commission on Environmental Quality's (TCEQ) Onsite Activity Reporting System (OARS). OARS is an online system for Authorized Agents (the agent in charge of permitting OSSFs for each county) to submit monthly reports about the number of OSSF permits requested and the number of complaints filed (complaints are typically filed by residents near the violating system). OARS reports are available as a yearly summary from 1992 to present. Using this method for estimating the percent of OSSF failure based on complaints reveals a less than 2% annual failure rate. Unfortunately, the data in OARS are not well updated and, likely, incomplete; also, since the majority of an OSSF unit is located underground, many system failures go unnoticed and unreported. They would, therefore, not be documented in OARS.

Another method for estimating failures is based on soil properties and assumed loadings from the homes. A 1978 study by Hydroscience Inc. used this approach to estimate non-point source contamination from OSSFs in their Southeast Texas study area (Hydroscience Inc., 1978). The study found that the soils of Southeast Texas are generally considered limited for use in OSSFs and that, because of this, many of the systems may be failing or performing as "open-ended" systems. An "open-ended" system is one that effectively discharges its septic tank effluent directly to a surface water or other above ground receiving body (a drainage ditch, for example). These systems

skip the treatment component of the drain field entirely and, therefore, have little or no bacterial treatment. Findings of the Hydroscience study estimate that the percent of "open-ended" septic systems in the study area were generally on the order of 50%, with estimates up to 90% in certain areas (Hydroscience Inc., 1978).

Lastly, a 2002 document by the U.S. Environmental Protection Agency (USEPA), "Onsite Wastewater Treatment Systems Manual", notes that no organizations formally document OSSF failure rates in the country. In an attempt to approximate a general rate, the report attempts to estimate OSSF failures in 1999 for 28 states (definitions of failure varied from state to state). Results of this attempt show that OSSF failure rates in the State of Texas range from 10-15% of systems (USEPA, 2002). Failures in other states range from <1 to 70 percent.

Surface Water Contamination from Failed OSSFs

Surface water contamination from failed OSSFs is likely to occur in one of two ways: directly or through contaminated groundwater. An example of direct application is the "open-ended" system. In an "open-ended system" the septic tank effluent could be directly deposited into the surface water or might outlet to an above ground area where it then flows to the surface water as overland runoff. Otherwise, bacteria may contaminate a groundwater source, which flows into a surface waterbody and contaminates the surface water.

A limited number of field studies have been done to research the likelihood of contamination of shallow groundwater aquifers from failing OSSFs. These studies concentrate on certain soil types, under specific loading and environmental conditions, which makes their findings difficult to generalize and apply directly to the Copano Bay study area. However, there are some patterns that emerge that we can use to develop an estimation of the likelihood of shallow groundwater contamination due to OSSF failure in our study area. Results of this estimation can then be used to discuss surface water contamination.

One common finding of the field studies is that the movement of coliforms under unsaturated flow conditions is much more limited than that under saturated flow (Hagedorn et al., 1981). In unsaturated flow, aerobic conditions can occur and longer residence times are present; death of the microorganisms, therefore, results in lower concentrations. Under saturated flow, studies show that bacterial concentrations reduce as water moves both laterally and vertically away from the drain field (Reneau and Pettry, 1975; Stewart and Reneau, 1981). The potential for aerobic conditions, however, is lost.

The physical removal (or filtering) of bacteria out of the groundwater is the largest limitation to its movement away from the drain field. Many studies show a significant reduction of bacterial levels in the first tens of meters of movement. However, some studies have shown that bacteria can move up to 830 meters in sand and gravel formations and survive for over 30 days (Hagedorn et al., 1981). Adsorption is

also shown to play a role in removing bacteria from groundwater and becomes more effective in soils with increased clay content (Hagedorn et al., 1981).

OSSFs IN THE COPANO BAY WATERSHED

Number of OSSFs

Up through 1990, the U.S. Census tracked the number of households using OSSFs per county across the nation. Since that time, however, the Census has no longer asked for that information. As discussed above, for the years 1992 to present, the TCEQ OARS has records of the number of OSSF permits requested per county. As also mentioned, however, OARS data are incomplete and there are many years when no data was reported for the counties of interest. To approximate the number of OSSFs per county in 2007, we combined the 1990 Census data with an estimated number of OSSFs built since that time. The estimate for 1990 to present was based on the reported average number of permits requested per year, multiplied by 18 years (the number of years from 1990 to 2007). Table C1 summarizes the results.

Table C1: Number of Reported OSSFs in Counties of Study Area

County	# of OSSFs in 1990	Years of Data in OARS	Avg # of Permit Requests per Year	Estimated # of OSSFs installed from 1990-2007	# of OSSFs in 2007
Aransas	6,456	16	246.7	4,441	10,897
Bee	3,859	17	54.3	977	4,836
Goliad	1,898	10	139.9	2,518	4,416
Karnes[1]	1,765	11	36.3	653	2,418
Refugio	1,033	13	22.1	397	1,430
San Patricio	5,722	16	130.2	2,343	8,065

[1] More complete data were provided by Ms. Sharon Chesser of Karnes County, which were used in this study.

Much of the land in the study area is rural. It is, therefore, likely that a number of OSSFs are installed every year without a permit. Discussions with the Authorized Agents in the study area counties confirm that the presence of un-permitted and, therefore, uncounted OSSFs, are in use. Also, there are a number of homes in the study area that are used as seasonal residences or otherwise are vacant for a portion of the year. A previous study in this watershed estimated that only 64 to 85% of the OSSFs in the study area are actively in use (Gibson, 2006). Due to the lack of accurate data on these topics, we assumed that these categories cancel each other out and the estimated number of OSSFs in Table C1 is reflective of the actual number of active (permitted or non-permitted) OSSFs in the counties of the study area in 2007.

To calculate the number of OSSFs in the watershed we first determined the area of each county that is classified as low and high density residential (LULC 21 and 22, respectively). We then calculated the density of OSSFs per residential area for each county. Each county's area of LULC 21 and 22 in the watershed was then used to

compute the total number of OSSFs in the watershed on a countywide basis. According to this calculation, the total number of OSSFs in the Copano Bay watershed in 2007 was 18,628.

Table C2: Number of OSSFs in the Copano Bay Watershed

County	# of OSSFs	Density of OSSFs in LULC Type 21 and 22 (#/km^2)	Area of LULC 21 and 22 in Watershed (km^2)	# of OSSFs in Copano Bay Watershed
Aransas	10,897	774.9	12.1	9,378
Bee	4,836	342.6	14.1	4,814
Goliad	4,416	1,837.0	0.3	532
Karnes	2,418	341.5	0	0
Refugio	1,430	185.7	6.6	1,220
San Patricio	8,065	278.4	9.6	2,685

Aransas and Refugio Counties have a number of OSSFs that are clustered together in development (sub-divisions, RV parks, and businesses) immediately around the bay. The number of OSSFs associated with these developments is estimated by the TX Department of State Health Services (DSHS) in their Bay Sanitary Surveys and annual updates. According to the 2006 and 2007 reports, Refugio County has 304 OSSFs in these developments and Aransas county has 1,875 (DSHS, 2006; DSHS, 2007). These OSSFs are assigned to each individual sub-division, recreational vehicle (RV) park, or business around the bay; the remaining OSSFs (16,449 in total) are evenly distributed among the LULC 21 and 22 in the upper watershed.

Study Area Soils

As mentioned, the type of soil at a site greatly affects an OSSFs ability to properly remove the pollutants that are emitted from the septic tank. Data from the Natural Resources Conservation Service (NRCS) Soil Survey Geographic Database (SSURGO) was used as the source of soil information for our work. Figure C2 shows the main soil categories in the SSURGO coverage for the Copano Bay watershed. It also shows the communities immediately around Copano Bay where OSSFs are used. OSSFs in the area away from the bay are not represented on the map.

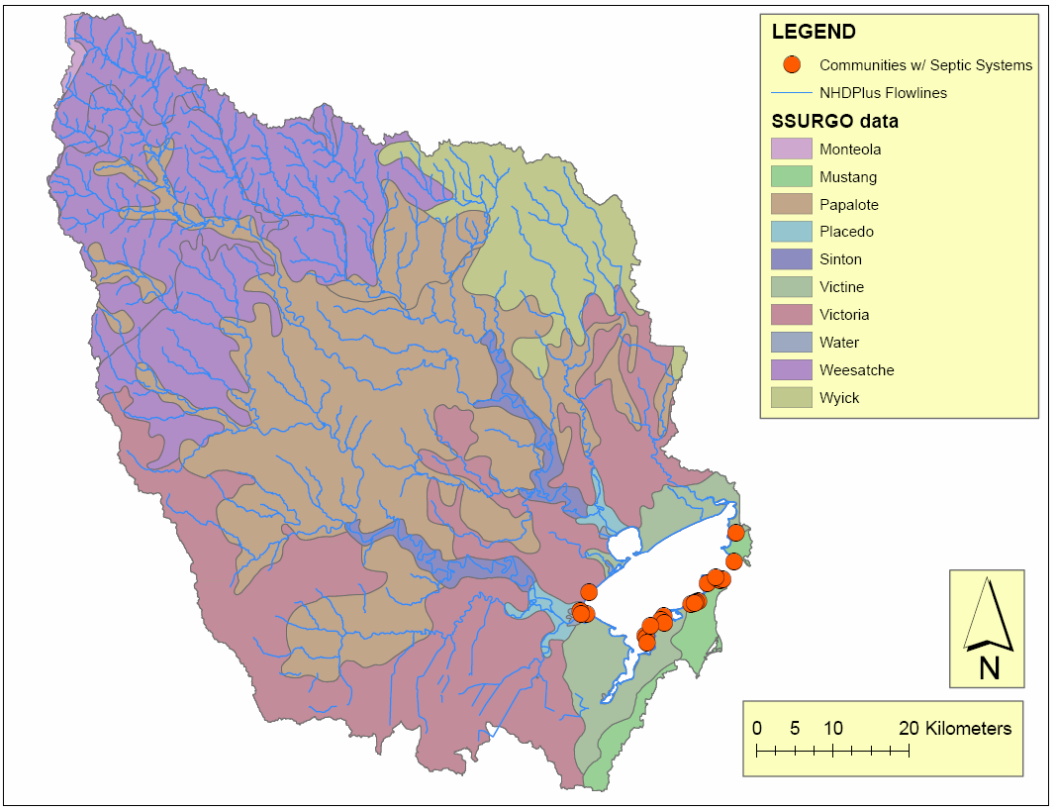


Figure C2: Soils in the Copano Bay Watershed

As part of their assessment, the NRCS rates soils for a number of uses, including their use as septic tank absorption fields. The septic tank absorption field rating concentrates on the soil at 24 to 72 inches of depth, assuming that this is the active zone of leaching and treatment (the infiltration and vadose zones, as discussed above). If the soil has a restrictive zone at a shallower depth than 72 inches, the depth of the restrictive layer is used as the bottom of evaluation. Reports on soil uses are available on a countywide basis online at the NRCS Web Soil Survey (Soil Survey Staff, 2008b). Table

C3 summarizes the septic ratings for the main categories of soil found in our study area. The majority of the soils are rated as "very limited" for use in septic disposal; one is rated as "somewhat limited". Reasons for limitation include slow water movement (which could lead to flooding or a high water table), depth to saturated zone, flooding, and seepage of the bottom soil layer.

Table C3: Soil Ratings for Septic Tank Absorption Fields – Study Area

Soil Category	Rating Class for OSSF Absorption Field	Limiting Features for Rating
Mustang	Very limited	Flooding Seepage, bottom layer Depth to saturated zone Filtering capacity
Victine	Very limited	Slow water movement Depth to saturated zone
Victoria	Very limited	Slow water movement
Papalote	Very limited	Slow water movement
Sinton	Very limited	Slow water movement Flooding Seepage, bottom layer
Wyick	Very limited	Slow water movement Depth to saturated zone
Weesatche	Somewhat limited	Slow water movement
Monteola	Very limited	Slow water movement

In the early 2000s, TCEQ instituted new OSSF regulations that require non-conventional OSSFs to be used in areas with limited ratings for septic system use. Non-conventional systems are designed to overcome the limiting features of the soil by using a lower septic effluent application rate or increasing the distance between the drain field and the water table by placing the field in a mound above the ground. The necessity of

installing a non-conventional system is determined on a site-by-site basis, as determined in a site assessment performed by a trained professional. Though many of the areas in the Copano Bay watershed have limiting soils and likely require non-conventional systems to be installed (under the current regulations), the vast majority of OSSFs in the area are conventional (OARS shows that the applications for non-conventional systems began as recently as 1998). For our work, we assumed that the number of OSSFs in the study area designed to overcome the limiting soils is insignificant. All OSSFs are subject to the same failure rates and performance assumptions.

Study Area Groundwater Table

A common cause of septic system failure is a shallow groundwater table. Research shows that between 2 and 5 feet of unsaturated, aerobic soil is necessary to provide adequate bacteria removal (Hagedorn et al., 1981; USEPA, 2002). Research also shows that the height of the groundwater table can be more influential in the failure of an OSSF than the loading rate to the system (Cogger et al., 1988). According to Texas regulations, conventional OSSFs must have at least 24 inches of vertical distance between the bottom of the drain field and the groundwater table.

Estimates of the groundwater table in the study area are made from Texas Water Development Board (TWDB) well records, information in the TCEQ Leaking Petroleum Storage Tanks (LPST) database, and conversations with personnel in the area. TWDB wells in the Copano Bay study area are typically not drilled into the upper aquifer, since

this water (especially in the zone immediately adjacent to the bay) is too saline for many uses. The majority of wells drilled in the area terminate in the deeper, freshwater aquifers. Since the deeper aquifers are not representative of the water table, they cannot be used to estimate water table depth. As a secondary source of data, the TCEQ LPST database was used. Wells in this database are typically located in the upper aquifer, since their purpose is to remove contamination that spilled into that zone. Twenty-one wells in the TCEQ LPST database were found adjacent to the bay; the average depth of the watertable in these wells is 3.7 feet below the ground surface.

In the upper watershed area, seven TWDB wells were found in the upper aquifer with records ranging from 1940 to 1967. The average water depth in these wells is 6.5 feet below the surface. To supplement this information, I spoke with a representative of the Refugio county Groundwater Conservation District, who estimated that water levels in the upper watershed range from 8 to 14 feet below surface (Engelking, 2009).

Estimated Impact of Failing OSSFs in the Study Area

To estimate the impact of failing OSSFs in the Copano Bay watershed, we first estimated the number of OSSFs failing on a mean annual basis. We then used findings from previous research to estimate the potential impact that each failing system could have on the surface waters of our study area. To perform the analysis, the OSSFs of the Copano Bay watershed were split into two separate categories: those immediately surrounding the bay and those away from the bay.

OSSFs immediately surrounding the bay are subject to a much higher groundwater table than are those in the upper watershed (approximately 4 feet versus 7 to 14 feet, as discussed above). Given the importance of maintaining a sufficient vertical distance between the drain field and the saturated zone, the likelihood of failure in the systems surrounding the bay is estimated to be much higher than those in the upper watershed. Considering the findings of the Hydroscience and USEPA reports on failure rates, we estimate the likelihood of failure in OSSFs surrounding Copano Bay at 50% - the lower estimate in the HydroScience report. Failures in the area away from the bay (i.e., the upper watershed) are estimated at 15%, the upper end of the range from the USEPA report.

Table C4: Assumed OSSF Failure and Loading Rates

Location	Assumed Failure Rate	Assumed % of Load Transmitted to Surface Water
OSSFs immediately surrounding Copano Bay	50%	50%
OSSFs up-gradient from Copano Bay	15%	20%

Failure of an OSSF can result in many outcomes that impact surface waters; we will address three of these possibilities. The first scenario occurs when the septic tank effluent is incompletely treated in the drain field and pollutes the shallow groundwater below it. This shallow groundwater can then pollute surface waters through their interactions. A second scenario is that septic tank effluent could be released directly to a

waterbody or to a ditch that drains to a waterbody (i.e., the "open-ended" system). In the third scenario, the effluent could pool on the ground surface and enter a surface waterbody as runoff.

Each of these outcomes has the potential to contaminate surface waters with bacteria. Of these scenarios, the most devastating is contamination due to "open-ended" systems that by-pass the treatment of the drain field altogether. In this scenario (largely) untreated wastewater is deposited directly into a waterbody. Contamination of a waterbody by pooled septage is the second most concerning scenario, followed by degradation due to interactions with polluted groundwater. Contamination due to groundwater interaction is not thought to be as much of a concern due to the studies that show that bacteria are effectively removed as water moves away from the drain field. It is noted, however, that bacteria have been shown to travel great distances under certain conditions, including the movement through macropores in the geological formation (Hagedorn et al., 1981).

Given the proximity of the OSSFs immediately surrounding the bay to the waterbody, the likelihood of an "open-ended" system failure or of septage entering as runoff is much greater than for the OSSFs in the upper watershed. The assumed percent of load transmitted to surface waters from failed OSSFs around the bay is, therefore, estimated at 50% while that for OSSFs in the upper watershed is estimated at 20%. These estimates are made solely as an "educated guess", as better information is not available at this time.

Appendix D: First Order Analysis of Uncertainty

First Order Analysis of Uncertainty

By: Stephanie L. Johnson

BACKGROUND

The First Order Analysis of Uncertainty approach quantifies the variance in a dependent modeling variable due to parameter uncertainty, while ignoring the modeling and natural uncertainty in the result. Thus, the analysis assumes that modeling equations properly reflect the relationship between the dependent and independent variables. The mean of the dependent variable is a function of the mean of the independent model inputs. The variance of the dependent variable is a function of the variance of each of the independent variables, the impact that a change in the independent variables would have on the dependent variable, and any correlation between the independent variables (Chow et al., 1988; Kapur and Lamberson, 1977).

Modeling Equations

The governing equations of the TMDL Balance model are a watershed loading equation (applied in tidal and non-tidal segments) and the tidal prism equation. For this analysis we are concentrating on the variance in loading from the watershed, which is described by Equations 4.1 through 4.3 in the dissertation text and repeated here (as Equations D1 through D3) for convenience. Loading in the freshwater river sections is calculated as

$$L_f = \sum_{i=1}^{I} q_i c_i * e^{-k\tau_i} + \sum_{j=1}^{J} q_j c_j * e^{-k\tau_j} \quad \text{(D1)}$$

Where: L_f = mean annual freshwater bacterial load (CFU/yr)

q_i = mean annual flow of water from point source *i* (m^3/yr)

c_i = expected mean concentration of bacteria from point source *i* (CFU/m^3)

k = first-order bacterial decay coefficient (yr^{-1})

τ_i = residence time from point source *i* to modeled location (yr)

q_j = mean annual flow of water from nonpoint source *j* (m^3/yr)

c_j = expected mean concentration of bacteria from nonpoint source *j* (CFU/m^3)

τ_j = residence time from nonpoint source *j* to modeled location (yr)

Tidal rivers are modeled as a series of completely stirred tank reactors as

$$L^* = Q^* \frac{L_f}{Q^* + kV} \quad \text{(D2)}$$

Where: L^* = mean annual bacterial load in the tidal river segment (CFU/yr)

Q^* = mean annual flow of tidal river segment (m^3/yr)

V = mean annual volume of tidal river segment (m^3)

The total amount of bacteria leaving the watershed and entering Copano Bay is then the sum of the load entering through the Aransas and Mission Tidal River segments and that entering from the land draining directly into the bay.

$$L_w = \sum L^* + L_d \quad \text{(D3)}$$

Where: L_w = mean annual bacterial load entering Copano Bay from the watershed (CFU/yr)

L_d = $\sum L_f$ for all non-tidal rivers and overland flow that drain directly into Copano Bay (CFU/yr)

ANALYSIS

Equations to Calculate Variance

The First Order Analysis of Uncertainty estimates the variance in the dependent variable as a function of the variance of each of the independent variables in the model. In this case, the independent variables are mean annual flow from point and nonpoint sources, concentration of bacteria from point and nonpoint sources, travel times through the watershed, and the first-order bacterial decay rate. The data available for this analysis are quite limited. For our purposes, we chose to use information collected during the intensive sampling discussed in Chapter 3 and historic flow data at the USGS gauge stations to quantify a portion of the uncertainty in modeling results due to the variance in concentrations and flows. Other uncertainties are ignored in this analysis. Also, it is assumed that the available data do not well represent the variance in loads from point sources. Point sources constitute loadings from wastewater treatment plants (with, potentially, more controlled bacterial concentrations and less variable flows) and failing septic systems/waterbird colonies around the bay. Point source loads are not a function

of the variation in in-stream flows and might experience more or less variation in bacterial concentrations than nonpoint sources. Focusing only on the variance in bacterial concentrations and flow from nonpoint sources in the watershed, Equation D1 becomes

$$L_f = \sum_{j=1}^{J} q_j c_j * e^{-k\tau_j} \quad \text{(D4)}$$

Where: L_f = mean annual freshwater bacterial load (CFU/yr)

q_j = mean annual flow of water from nonpoint bacterial source *j* (m^3/yr)

c_j = expected mean concentration of bacteria from nonpoint source *j* (CFU/m^3)

k = first-order decay coefficient (yr^{-1})

τ_j = residence time from nonpoint bacterial source *j* to modeled location (yr)

The variance in the loading from the freshwater rivers as a function of the dependent variables is then computed as

$$s_{L_f}{}^2 \approx \sum_{j=1}^{J} \left(\frac{dL_f}{dc_j}\right)^2 s_{c_j}{}^2 + \sum_{j=1}^{J} \left(\frac{dL_f}{dq_j}\right)^2 s_{q_j}{}^2 + 2\sum \left(\frac{dL_f}{dc_j}\right)\left(\frac{dL_f}{dq_j}\right)\rho_{c_j,q_j} s_{c_j} s_{q_j} \quad \text{(D5)}$$

Where: $s_x{}^2$ = variance in variable *x*

ρ_{c_j,q_j} = coefficient of correlation between c_j and q_j

Since the coefficient of variation (CV) = $s_x/\bar{x}_x$ and the covariance of two variables x_1 and x_2 [$COV(x_1, x_2)$] = $\rho_{x1,x2}s_{x1}s_{x2}$, D5 equates to

$$s_{L_f}{}^2 \approx \sum\left[q_j e^{-k\tau_j}\right]^2\left(CV_{c_j}c_j\right)^2 + \sum\left[c_j e^{-k\tau_j}\right]^2\left(CV_{q_j}q_j\right)^2 + 2\sum\left[\left(q_j e^{-k\tau_j}\right)\left(c_j e^{-k\tau_j}\right)\right]COV(c_j, q_j) \tag{D6}$$

This equation quantifies the variance in the freshwater load of bacteria as the sum of the effect of the variance in concentration, plus the effect of variance in the flow, plus the effect of variance due to the correlation between these variables. Similarly, variance in the bacterial loading exiting the tidal rivers is calculated as

$$\begin{aligned} s_{L^*}{}^2 &\approx \sum\left(\frac{dL^*}{dL_f}\right)^2 s_{L_f}{}^2 + \sum\left(\frac{dL^*}{dQ^*}\right)^2 s_{Q^*}{}^2 + 2\sum\left(\frac{dL^*}{dL_f}\right)\left(\frac{dL^*}{dQ^*}\right)\rho_{L_f,Q^*}s_{L_f}s_{Q^*} \\ &= \sum\left(\frac{Q^*}{kV+Q^*}\right)^2 s_{L_f}{}^2 + \sum\left(\frac{kL_fV}{(kV+Q^*)^2}\right)^2\left(CV_{Q^*}Q^*\right)^2 \\ &\quad + 2\sum\left(\frac{Q^*}{kV+Q^*}\right)\left(\frac{kL_fV}{(kV+Q^*)^2}\right)s_{L_f}s_{Q^*} \end{aligned} \tag{D7}$$

where, in this case, V is the total tidal volume that the load must travel through before it enters Copano Bay (for example, the V for the freshwater load that enters into the first segment of the Aransas Tidal River and travels through the entire segment to the bay is modeled as $4.8\text{x}10^6$ m^3). Since load is a direct function of flow, the correlation between L_f and Q^* (ρ_{L_f,Q^*}) is modeled as one. Finally, the variance in the total loading to Copano Bay from tidal rivers and overland runoff are computed as

$$s_{L_w}{}^2 \approx \left(\frac{dL_w}{dL_d}\right)^2 s_{L_d}{}^2 + \sum\left(\frac{dL_w}{dL^*}\right)^2 s_{L^*}{}^2 = \sum\left(\frac{dL_w}{dL_f}\right)^2 s_{L_f}{}^2 + \sum\left(\frac{dL_w}{dL^*}\right)^2 s_{L^*}{}^2 = \sum s_{L^*}{}^2 + \sum s_{L_f}{}^2 \quad (8)$$

since $\left(\frac{dL_w}{dL_f}\right) = \left(\frac{dL_w}{dL_t}\right) = 1$. In this case, $\sum s_{L^*}{}^2$ represents the variance of the loading from the Aransas Tidal River plus that from the Mission Tidal River. $\sum s_{L_f}{}^2$ is the sum of the variance in loadings from freshwater sources (i.e., small non-tidal rivers and overland flow) that drain directly into Copano Bay.

Calculating the Variance of Independent Variables

The variance in and correlation between streamflow and fecal coliform concentrations were computed from raw data. Mean daily flow values from the two main USGS gauging stations in the watershed (i.e., 08189700 Aransas River near Skidmore, TX and 08189500 Mission River at Refugio, TX) were used to analyze the expected variance in flows coming from the watershed. Table D1 summarizes the analysis, which reveals an average coefficient of variation of approximately 9.

Table D1: Summary Statistics for Mean Daily Streamflow at Main USGS Gauge Stations in Study Area

Station	Number of Samples	Mean (cfs)	Standard Deviation (cfs)	Coefficient of Variation
08189700	13,302	34.9	372.8	10.7
08189500	25,174	128.7	999.0	7.8
Average				***9.3***

Variance in fecal coliform concentrations was analyzed from the results of the targeted sampling plan in the watershed between September 2007 and October 2008, which is discussed in Chapter 3 of this dissertation. Table D2 show the summary statistics that were computed at each sampling site. Based on these data, an average coefficient of variation of approximately 2 is observed. This is similar to values reported in the literature, which are approximately 1.5 (Maidment, 1992). Therefore, the variance of fecal coliform from each nonpoint source in the watershed is computed based on a coefficient of variation of 2 and the modeled mean at that point.

Table D2: Summary Statistics for Fecal Coliform Concentrations at Sampled Sites

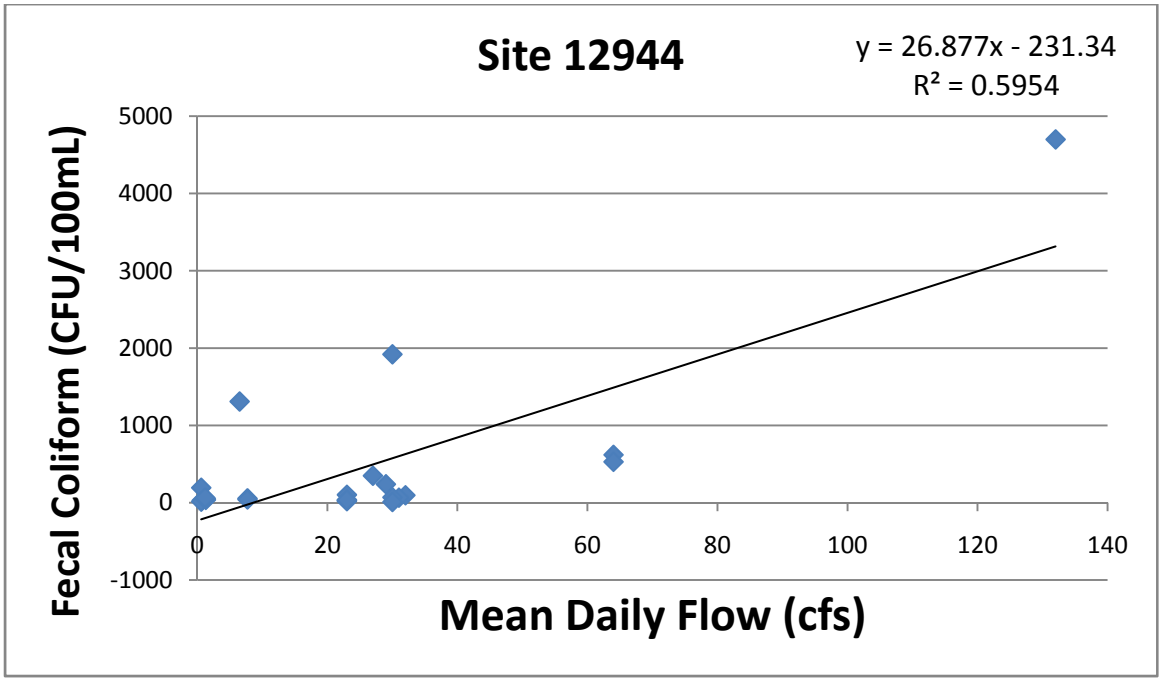
Site	**Number of Samples**	**Mean (CFU/100ml)**	**Standard Deviation (CFU/100ml)**	**Coefficient of Variation**
12932	18	418.6	811.9	1.9
12944	20	450.5	1058.1	2.3
12948	21	1288.7	2725.8	2.1
12952	20	691.8	2276.8	3.3
13660	11	1873	1600.4	0.85
20058	21	1600.5	4120.8	2.6
20059	9	56.6	68.9	1.2
20060	19	187.6	284.4	1.5
20061	9	69.1	129.9	1.9
20062	9	84.9	98.4	1.2
20063	20	232.3	367.2	1.6
20064	18	75	131.4	1.8
20065	19	503.6	1041.8	2.1
20066	15	630.1	1691.0	2.7
Average				***1.9***

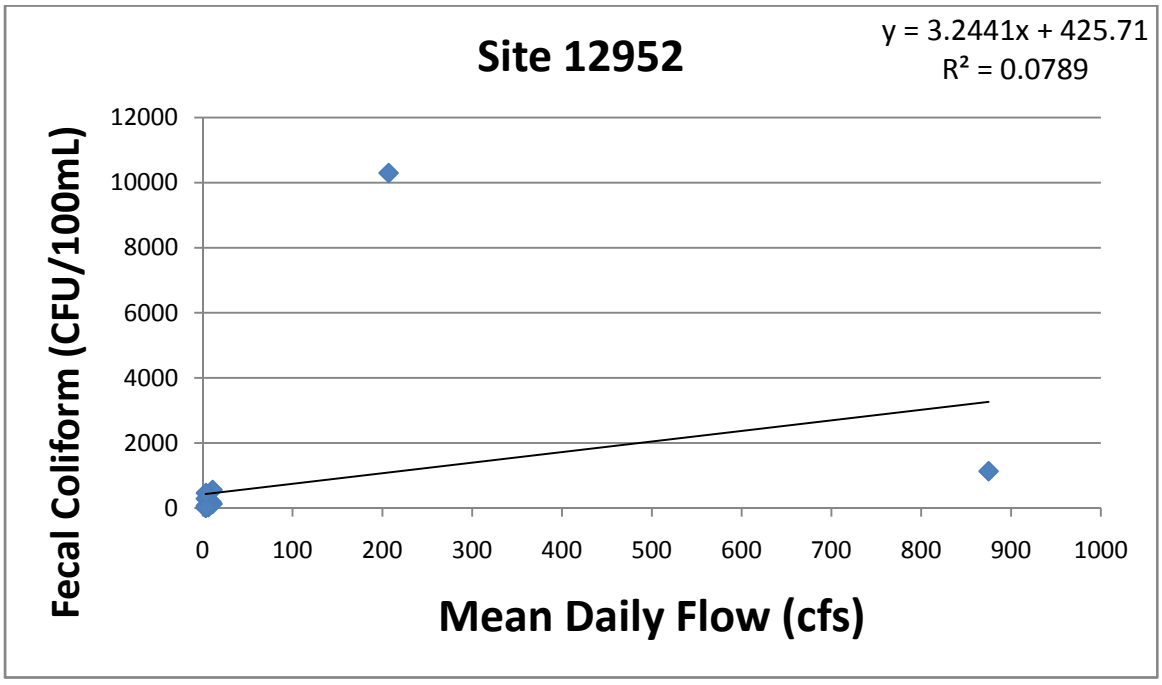
Correlation of Flow and Fecal Coliform Concentration

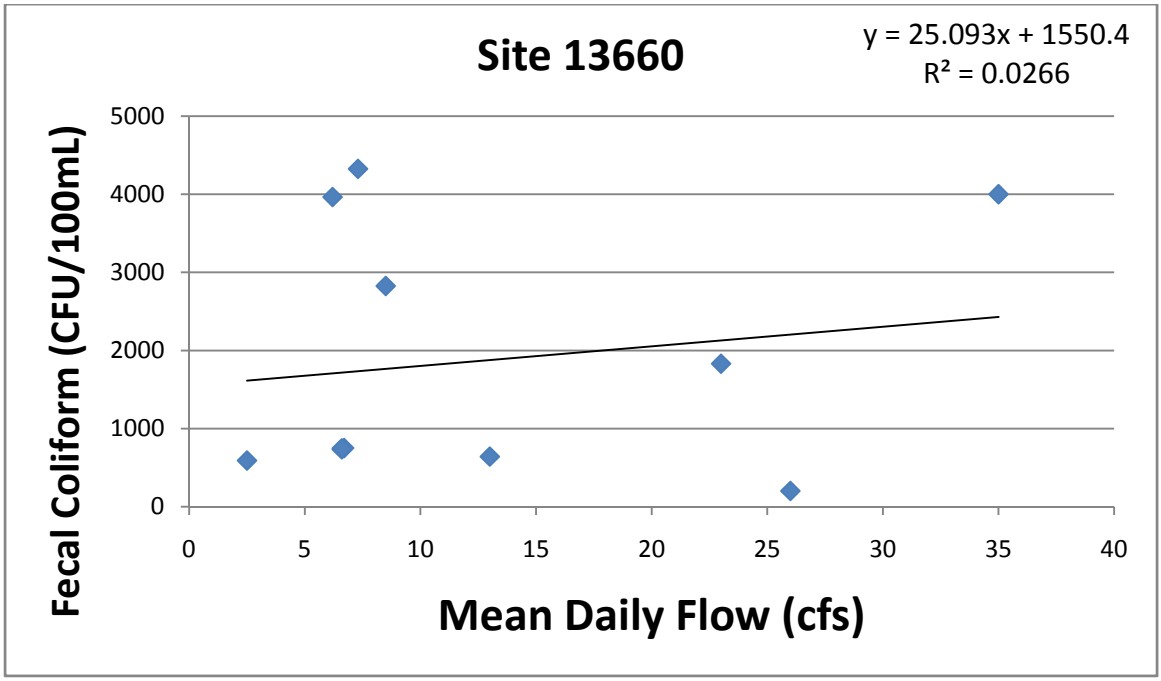
Four of the sites sampled during the targeted sampling effort are located at USGS gauging stations, which have mean daily flow values available. For this work, we computed the correlation between the mean daily flow and the fecal coliform concentrations at those sites during non-zero flow sampling events. Table D3 shows the results. Plots of the data follow the table. (Note that the R^2 values in the plots are equal to the square of the correlations presented in Table D3.) Results of this analysis show an average correlation of approximately 0.5 between these variables.

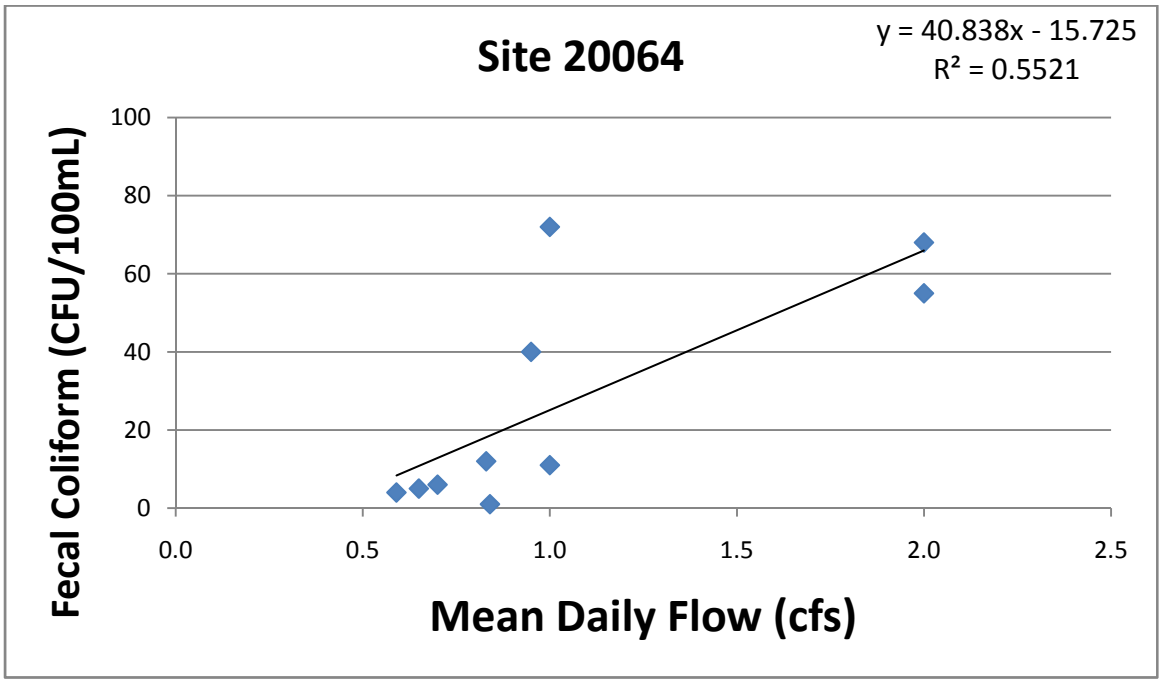
Table D3: Correlation between Sampled Fecal Coliform Concentrations and Mean Daily Streamflow at Sampling Sites

Site	**Correlation (R)**
12944	0.772
12952	0.281
13660	0.163
20064	0.743
Average	***0.480***


Site 12944
y = 26.877x - 231.34
R² = 0.5954
Fecal Coliform (CFU/100mL)
5000
4000
3000
2000
1000
0
-1000
0
20
40
60
80
100
120
140
Mean Daily Flow (cfs)


Site 12952
y = 3.2441x + 425.71
R² = 0.0789
Fecal Coliform (CFU/100mL)
12000
10000
8000
6000
4000
2000
0
0
100
200
300
400
500
600
700
800
900
1000
Mean Daily Flow (cfs)


Site 13660
y = 25.093x + 1550.4
R² = 0.0266
Fecal Coliform (CFU/100mL)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
30
35
40
Mean Daily Flow (cfs)


Site 20064
y = 40.838x - 15.725
R² = 0.5521
Fecal Coliform (CFU/100mL)
100
80
60
40
20
0
0.0
0.5
1.0
1.5
2.0
2.5
Mean Daily Flow (cfs)

Figures D1 to D4: Observed Relationship between Mean Daily Flow and Fecal Coliform Concentrations at Four Sampling Sites with USGS Gauge Stations

Results

The uncertainty analysis was run for the entire watershed, computing the variance in nonpoint source load due to variance in flow and expected fecal coliform concentrations. Table D4 shows the results of the analysis for four main loading calculations in the study area: the load from each tidal river to Copano Bay, the load from overland runoff directly into Copano Bay, and the total loading to Copano Bay.

Table D4: Results of the Nonpoint Source First Order Analysis of Uncertainty at Major Load Outlets in the Watershed

Modeled Variable	**Mean Annual Load (10^{15} CFU/yr)**	**St. Dev. in Modeled Load (10^{15} CFU/yr)**	**Coefficient of Variation**
Nonpoint Source Load from Aransas River Tidal to Copano Bay	0.66	4.15	6.30
Nonpoint Source Load from Mission River Tidal to Copano Bay	0.67	4.83	7.18
Nonpoint Source Load from Overland Flow Directly to Copano Bay	4.91	7.99	1.63
Overall Nonpoint Source Load from Watershed to Copano Bay	6.24	10.20	1.64

Appendix E: Modeling Bacterial Distributions for Use in Computing TMDLs

Modeling Bacterial Distributions for Use in Computing TMDLs

By: Stephanie L. Johnson

Introduction

The purpose of this exercise is to compute the distribution of bacterial concentrations that can occur in the modeled waterbodies (Mission Tidal River, Aransas Tidal River, and Copano Bay) while still meeting water quality standards. The analyses are performed on water quality data ranging from December 1999-November 2006, the time period used for the most recent 2006 TMDL assessment.

To compute future distributions in the waterbody, we assume that the current (observed) distribution of bacteria is reflective of future conditions. Therefore, when reducing the bacterial load to the waterbody, we simply reduce the distribution in magnitude; we do not change its shape. This assumption equates to assuming that the standard deviation of the natural log (ln) of the raw data (i.e., the slope of the distribution when plotted on a log-normal probability plot) is constant. We then plot the observed data on a log-normal probability plot (since the data are log-normally distributed) and "slide" the distribution down until the water quality criteria addressing the geometric mean, median, 75% (value that 75% of the concentration values are less than or equal to), and 90% concentrations are attained.

The methods assume that the seven years of discrete sample data used in the analysis are reflective of the underlying continuous population. Based on that assumption, the 75% concentration of the modeled data is assumed to be equal to the modeled 75th percentile. Additionally, since the data are log-normally distributed, by definition, the geometric mean of the data is equal to the median.

Tidal River Segments

Table E1 summarizes the statistics computed for the enterococci samples collected during the assessment period. As expected, the data exhibit a log-normal distribution for the concentrations in both the Aransas and Mission Tidal River segments. This is shown in the summary statistics in Table E1 and in the log-normal probability plots of the data shown in Figures E1 and E2. As shown in Table E1, the segments violate the bacterial water quality standard under both geometric mean and 75% conditions (highlighted in red in the table).

Table E1: Statistics for Enterococci Concentrations in Tidal River Segments (December 1999-November 2006)

Waterbody	Number of Samples	Geometric Mean	75% Value	Arithmetic Mean	Standard Deviation of ln(x)[1]
Aransas Tidal River (CFU/100ml)	23	115	590	908	2.03
Mission Tidal River (CFU/100ml)	28	67	150	266	1.39

[1] Where *x* denotes the sampled enterococci concentrations.

Figure E1 shows the Aransas Tidal River enterococci data plotted on a log-normal probability plot. The observed data points are indicated as blue diamonds. Note that the equation of the line through the observed data is $y = 115.14 * e^{2.03x}$, where the y-intercept of 115.14 colony forming units per one hundred milliliters (CFU/100ml) is the geometric mean (and, by definition, median) of the distribution. The slope of the line (2.03 CFU/100ml) represents the standard deviation of the natural log of the observed values.

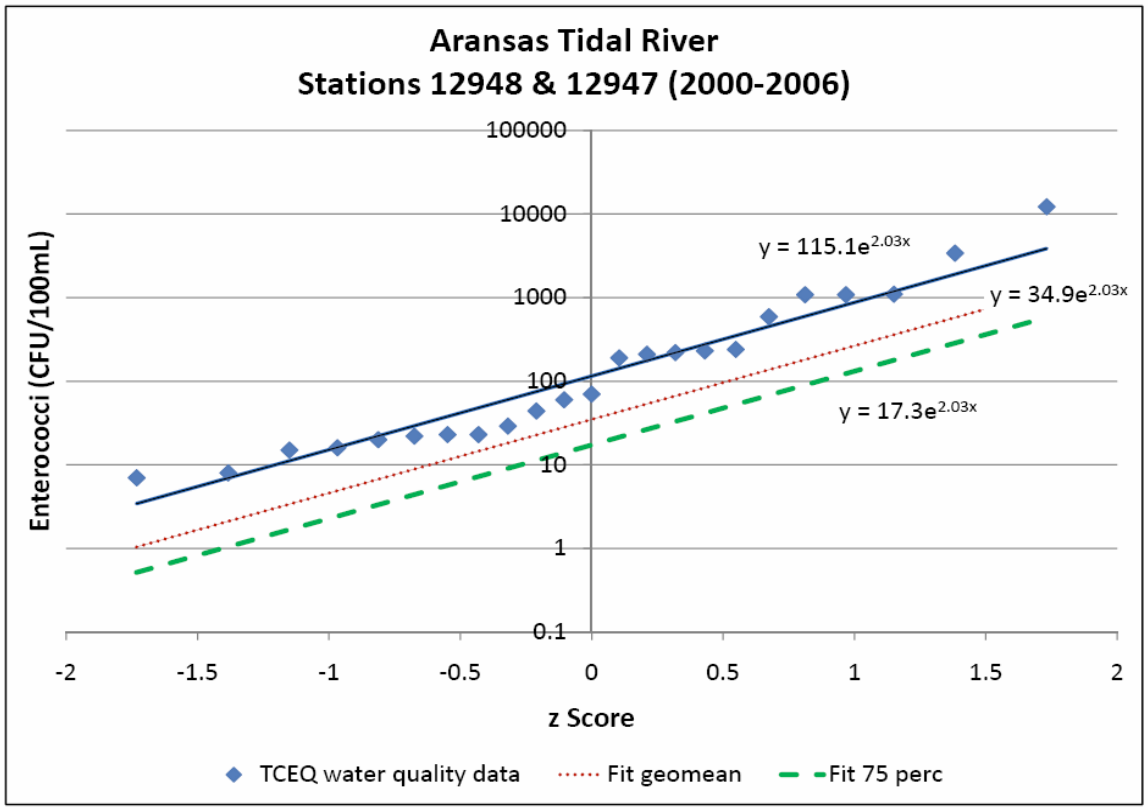


Figure E1: Observed and Modeled Distributions of Enterococci Concentrations in the Aransas Tidal River

To compute the distribution of bacteria needed to meet the water quality standard that applies to this river segment, we "slide" the observed distribution down on the plot until each water quality criterion is met. Again, the shape of the distribution (i.e., the slope of the line) remains constant, only the magnitude of the concentrations is reduced. The "Fit geomean" line, shown as a red dotted line in Figure E1, represents the distribution of maximum allowable enterococci concentrations while meeting the

geometric mean water quality criterion (i.e., geometric mean ≤ 35 CFU/100ml). The "Fit to 75 perc" line, shown as a green dashed line, indicates the allowable distribution when the 75% concentration criterion is attained (i.e., 75% of samples ≤ 89 CFU/100ml). Table E2 summarizes the statistics of each of the reduced distributions.

Table E2: Basic Statistics for Modeled Enterococci Concentrations in Tidal River Segments under Concentrations Regulated by the Water Quality Standards

Waterbody	Water Quality Standard	Geometric Mean	75th Percentile[1]	Arithmetic Mean
Aransas Tidal River (CFU/100ml)	Geometric Mean	34.9	178.8	275.1
Aransas Tidal River (CFU/100ml)	**75%**	**17.3**	**88.7**	**136.5**
Mission Tidal River (CFU/100ml)	**Geometric Mean**	**34.4**	**76.9**	**136.6**
Mission Tidal River (CFU/100ml)	75%	39.5	88.2	156.7

Note: Bolded scenarios are those that were recommended and used in modeling.

[1] 75th percentile is assumed to be equal to the 75% value in this analysis.

Note that the maximum allowable distribution modeled to meet the geometric mean water quality criteria is not in compliance at the 75% value. Since both water quality criteria must be met at once, this distribution is not satisfactory. The 75% distribution is more stringent and results in both criteria being attained. The maximum allowable concentration distribution modeled to meet the 75% water quality criteria is, therefore, recommended.

The same procedure is followed for the Mission Tidal River segment, as shown in Figure E3 and Table E2. In this case, the geometric mean condition is the more stringent reduction scenario. Therefore, for the Mission Tidal River, the distribution modeled to attain the geometric mean criteria is recommended.

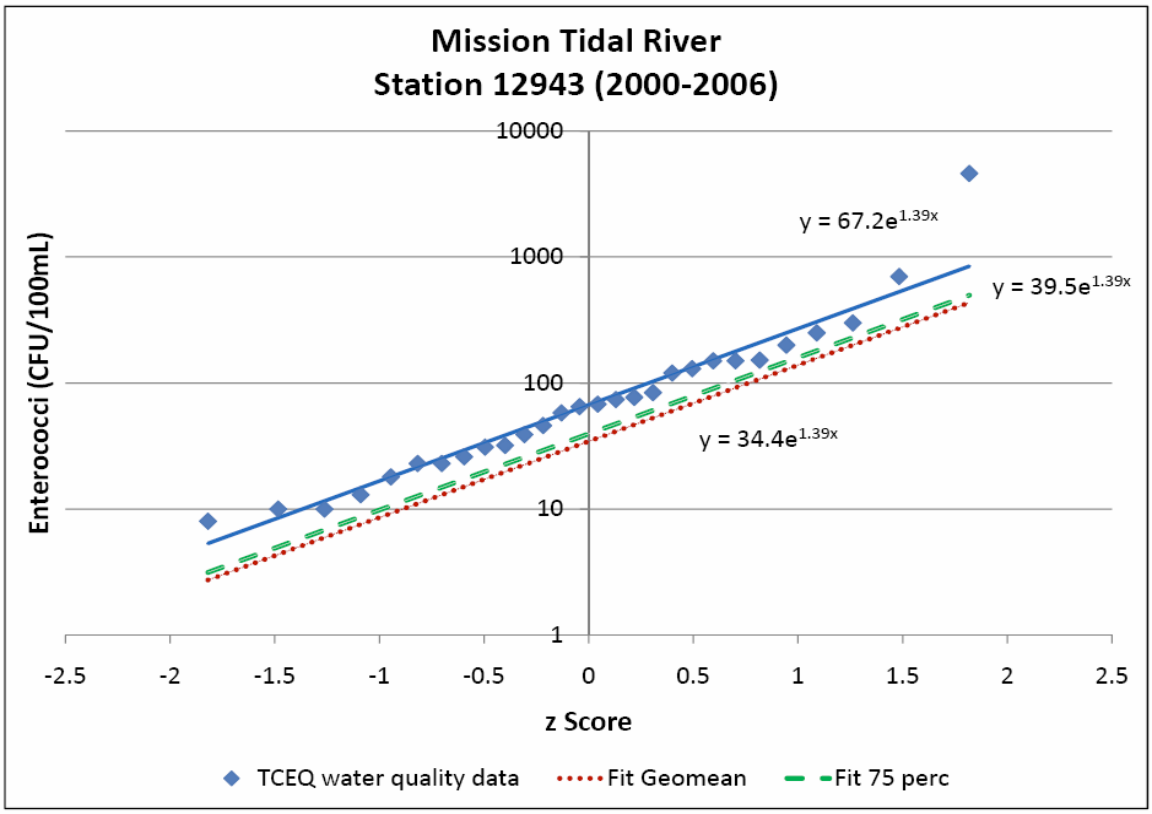


Figure E2: Observed and Modeled Distributions of Enterococci Concentrations in the Mission Tidal River

Copano Bay

A similar approach is taken to compute the distribution of maximum allowable bacterial concentrations in Copano Bay, based on historic water quality data. Recall, however, that the TMDL Balance water quality model addresses Copano Bay as a single waterbody (i.e., model inputs require the user to group the data from all the water quality sites together and then compute the statistics) while the State regulates each site separately. To account for this discrepancy, we assume that the relationship among the distributions of the individual sites and the whole bay will remain constant as the bacterial load into the bay is reduced. Therefore, by "sliding" the line representing the whole bay down on the plot we also "slide" the lines representing the distribution at each individual site down on a similar magnitude.

Table E3 shows the statistics for the observed fecal coliform concentrations at each of the sites in Copano Bay and for the bay as a whole. The five sites that violate the water quality standard are highlighted in red. Statistics for this analysis are computed using the "robust" regression on order statistics (ROS) approach, as outlined in Helsel (2005). This approach is taken to account for the large number of non-detect data in the sample group. Note also that the bay modeled as a single waterbody (i.e., single cell) meets the water quality standard.

Table E3: Basic Statistics for Fecal Coliform Concentrations at Violating Sites in Copano Bay and in Copano Bay as a Whole (December 1999-November 2006)

Site	Number of Samples	Median	90% Value	Arithmetic Mean	Standard Deviation of ln(x)
12945	15	37	118	66.2	1.28
13404	52	0.8	21	11.1	2.50
13405	14	6.5	290	80.3	2.36
14779	59	0.03	5	6.9	3.57
14780	37	1.1	13	2.5	1.30
14781	38	0.8	5	2.0	1.36
14782	38	0.003	1.9	4.0	4.86
14783	50	0.16	33	45.8	3.94
14784	41	0.21	5	4.6	2.82
14785	38	0.04	1.2	0.6	2.52
14786	38	2.8	17	6.0	1.28
14787	38	0.8	33	13.8	2.68
14788	38	0.5	79	69.9	3.81
14790	38	0.3	13	7.4	2.80
14792	38	0.3	110	115.0	4.53
14793	37	2.6	22	11.6	1.81
14797	29	0.7	49	22.1	3.10
Whole Bay	638	0.52	22	23.6	3.6

Figure E3 shows the fecal coliform concentration distributions for those sites that violate the water quality and for the bay as a whole (which includes data from violating and non-violating sites).

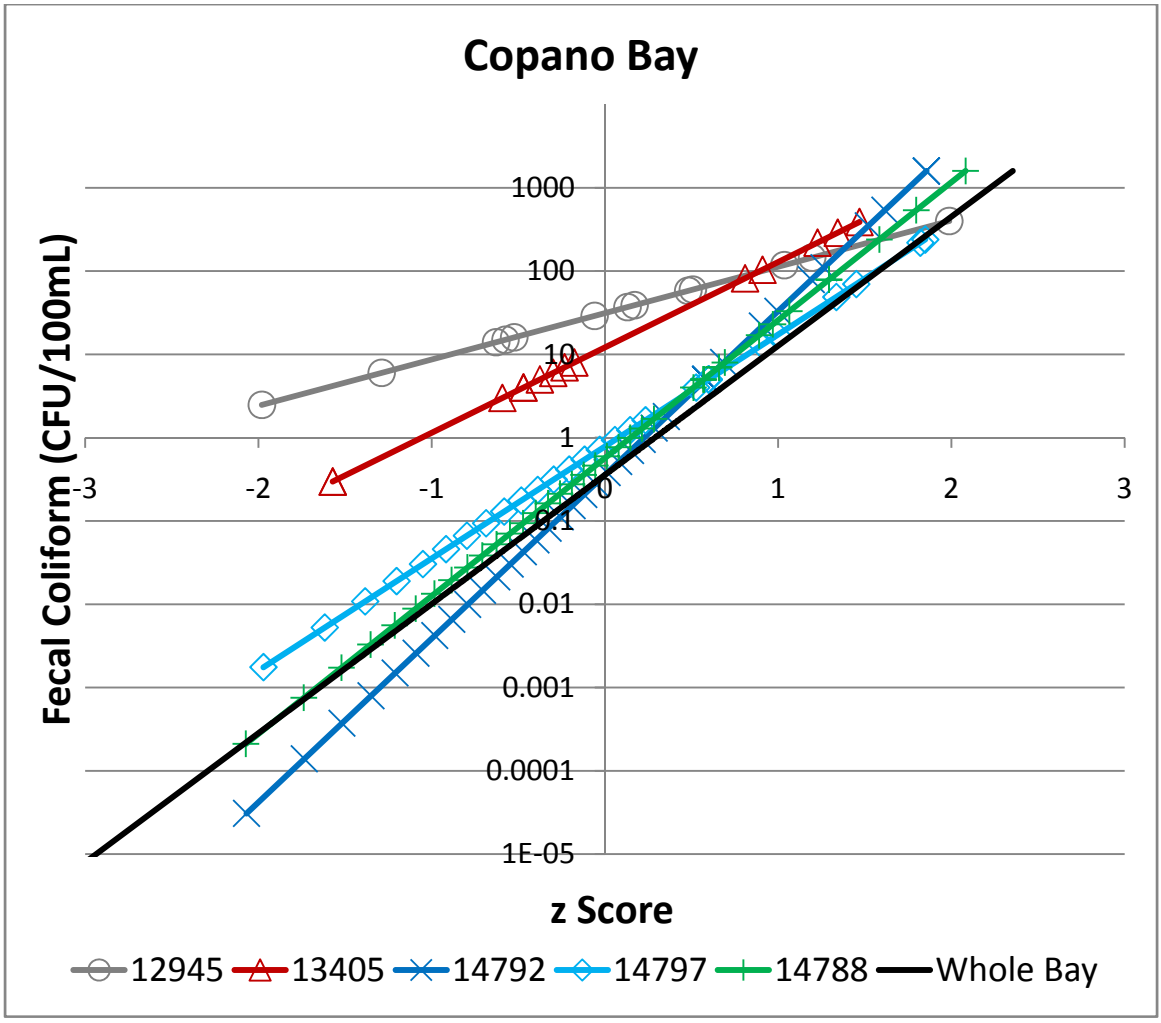


Figure E3: Observed Distributions of Fecal Coliform Concentrations at Sites that Violate Water Quality Standards in Copano Bay and in Copano Bay as a Whole

To model the distribution of maximum allowable fecal coliform concentrations for the bay as a whole, we "slide" all of the distributions down until the modeled distribution at every site (and, therefore, the whole bay) meets the water quality standard.

Figure E4 shows the maximum allowable concentration distributions under this scenario. The 90th percentile concentration at Site 13405 results in the largest concentration reduction and, therefore, dominates the analysis. Summary statistics of these results are given in Table E4.

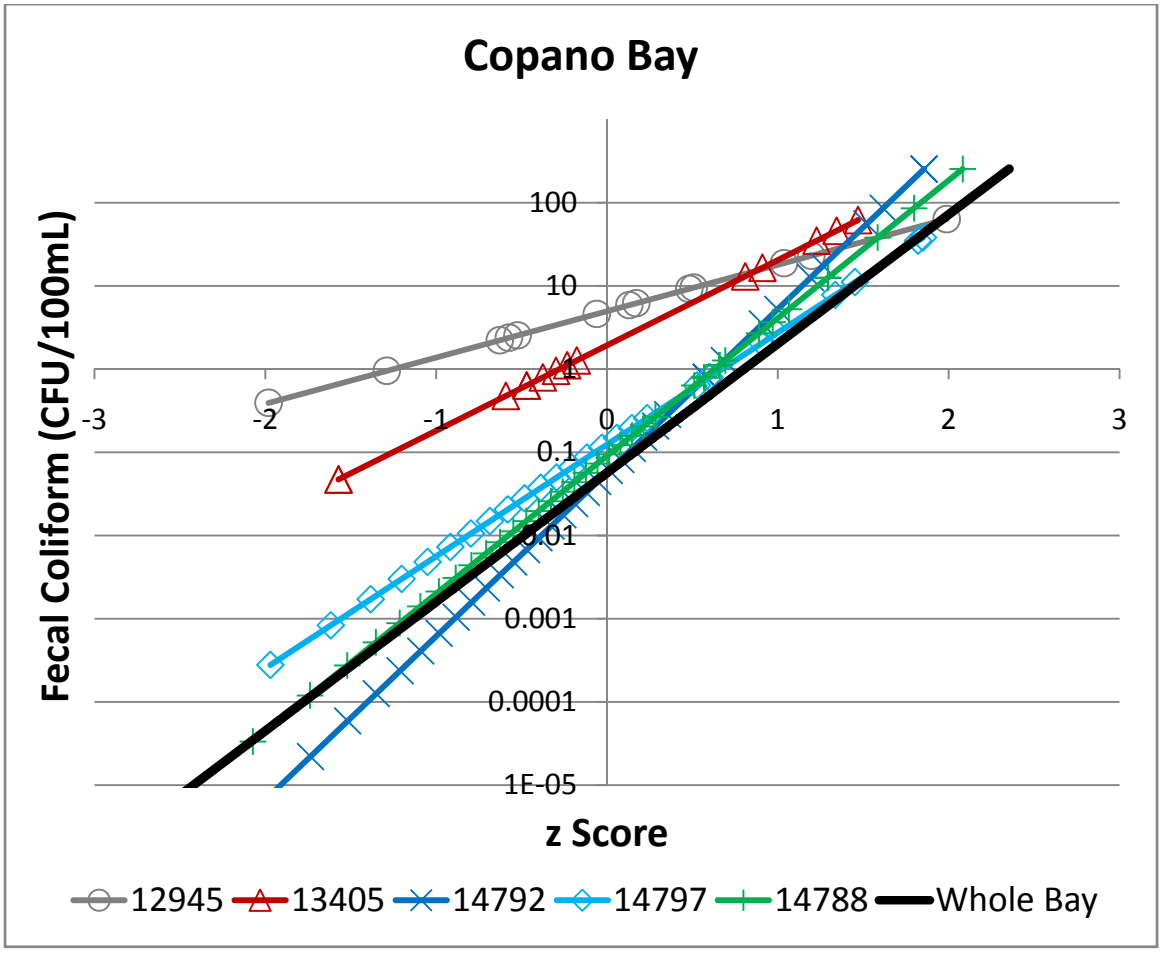


Figure E4: Modeled Distributions of Fecal Coliform Concentrations in Copano Bay

Table E4: Basic Statistics for Modeled Fecal Coliform Concentrations in Copano Bay under Concentrations Regulated by the Water Quality Standards

Site	Median	90th Percentile[1]	Arithmetic Mean
12945	5.0	21.3	10.5
13405	1.9	42.7	12.7
14792	0.06	28.9	18.3
14797	0.12	8.4	3.5
14788	0.09	12.5	11.1
Whole Bay	0.08	3.5	3.7

[1] 90th percentile is assumed equal to the 90% value in this analysis.

Appendix F: Model Verification and Sensitivity Analysis

Model Verification and Sensitivity

By: Stephanie L. Johnson

Introduction

The purpose of this appendix is to summarize the model verification and sensitivity analysis performed for the TMDL Balance model of mean annual bacterial loading in the Copano Bay watershed (discussed in Chapters 4 and 5 of this dissertation). The first portion of the appendix is a verification that increases in the nonpoint source loading in two different catchments in the watershed result in the anticipated change in loadings to Copano Bay. This verification confirms that the TMDL Balance model is performing correctly, passing and decaying loads as they move through the system. The second half of the appendix quantifies the impact that a change in selected model parameters will have on the results of the model under mean annual conditions. The outcome of this analysis shows which parameters have the greatest impact on model results.

Verification

Since TMDL Balance is a linear model, we can verify its operation by increasing the load in a single catchment in the watershed and tracking the impact of that increase as

the load moves downstream and into Copano Bay. As discussed in Chapter 4, the bacterial load in the non-tidal rivers of the watershed is computed as a function of upstream point and nonpoint sources and first-order bacterial decay, as shown in Equation F1.

$$L_f = \sum_{i=1}^{I} q_i c_i * e^{-k\tau_i} + \sum_{j=1}^{J} q_j c_j * e^{-k\tau_j} \quad \text{(F1)}$$

Where: L_f = mean annual freshwater bacterial load (colony forming units [CFU]/yr)

q_i = mean annual flow of water from point source *i* (m^3/yr)

c_i = expected mean concentration of bacteria from point source *i* (CFU/m^3)

k = first-order bacterial decay coefficient (yr^{-1})

τ_i = travel time from point source *i* to modeled location (yr)

q_j = mean annual flow of water from nonpoint source *j* (m^3/yr)

c_j = expected mean concentration of bacteria from nonpoint source *j* (CFU/m^3)

τ_j = travel time from nonpoint source *j* to modeled location (yr)

If the load from one of the nonpoint sources is increased (in this case, by Δl), the expected impact that increase will have on the load in the non-tidal river segment (ΔL_f) is computed as

$$L_f + \Delta L_f = \sum_{i=1}^{I} q_i c_i * e^{-k\tau_i} + \sum_{j=1}^{J} q_j c_j * e^{-k\tau_j} + \Delta l_x * e^{-k\tau_x} \quad \text{(F2)}$$

Where: ΔL_f = change in mean annual freshwater bacterial load (CFU/yr)

Δl_x = change in nonpoint source load in catchment x (CFU/yr)

τ_j = travel time from nonpoint source x to modeled location (yr)

Equation F2 simplifies to

$$\Delta L_f = \Delta l_x * e^{-k\tau_x} \quad \text{(F3)}$$

In this exercise, we use Equation F3 to compute the expected increase in freshwater loading from an increased load in the nonpoint source loading in one of the catchments. The anticipated ΔL_f is then compared to the output of the TMDL Balance model to verify that the model is working correctly.

This verification analysis was performed for two different catchments. The first catchment, (COMID) 5297665, is located on the Aransas River side of the watershed, as shown in Figure F1. Overland runoff from this catchment travels through one catchment segment, four non-tidal river segments, six tidal river segments, and into the bay. Under mean annual conditions, the travel time in the catchment and non-tidal river segments is modeled as 2.2 days (0.0059 years). The decay rate in these segments is 696 years^{-1}. The attributes of the tidal river segments are shown in Table F1. In this case, Equation F3 was used to compute the expected increase in loading in the non-tidal rivers. A similar exercise to that explained for non-tidal river loads in Equations F1 through F3 was then used to compute ΔL^* and ΔL_w, the expected increase in loadings in the tidal river segments and in Copano Bay.

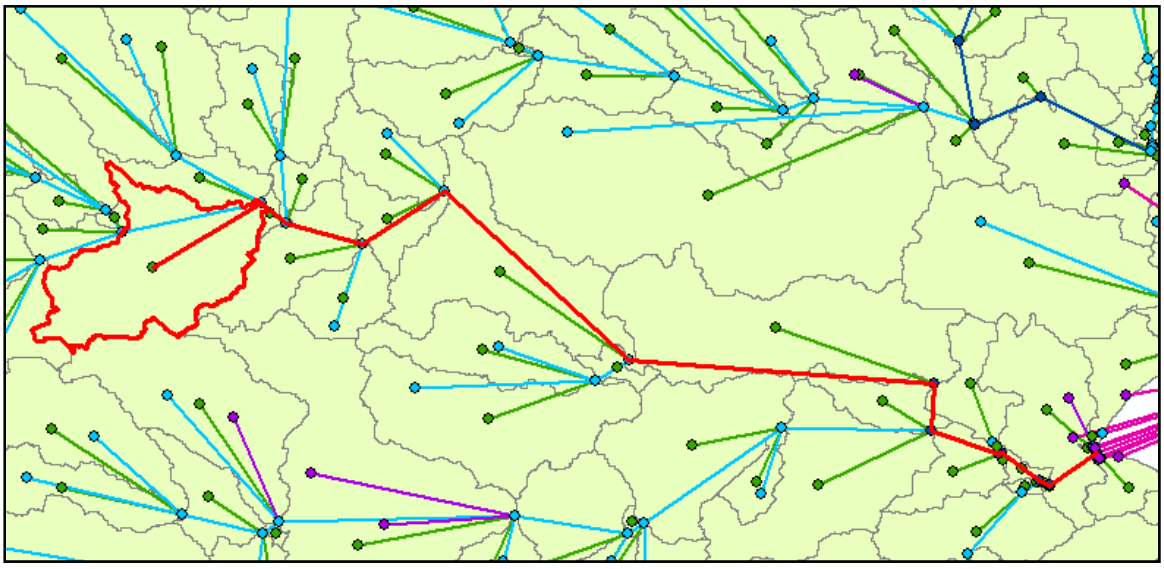


Figure F1: Catchment 5297665 Travel Path to Copano Bay

Table F1: Tracing the Increased Load from Catchment 5297665

Segment	Volume (m^3)	Flow Rate (m^3/yr)	Travel Time (years)	Decay Rate ($years^{-1}$)	Load into Segment (CFU/year)	Load out of Segment (CFU/year)
Catchment & Non-tidal	N/A	N/A	0.0059	696	$1.40x10^{15}$	$2.24x10^{13}$
Tidal: HydroID 1800	$3.4x10^{6}$	$1.08x10^{8}$	N/A	1060	$2.24x10^{13}$	$6.54 x10^{11}$
Tidal: HydroID 1798	$2.8 x10^{5}$	$1.16x10^{8}$	N/A	1060	$6.54x10^{11}$	$1.84 x10^{11}$
Tidal: HydroID 1790	$2.8 x10^{5}$	$1.95x10^{8}$	N/A	1060	$1.84x10^{11}$	$7.29 x10^{10}$
Tidal: HydroID 1782	$2.1 x10^{5}$	$1.97x10^{8}$	N/A	1060	$7.29x10^{10}$	$3.40 x10^{10}$
Tidal: HydroID 1769	$3.9 x10^{4}$	$2.26x10^{8}$	N/A	1060	$3.40x10^{10}$	$2.87 x10^{10}$
Tidal: HydroID 1767	$1.0 x10^{4}$	$2.26x10^{8}$	N/A	1060	$2.87x10^{10}$	$2.74 x10^{10}$

In this scenario, the mean annual nonpoint source loading from catchment 5297665 was increased from $1.6x10^{15}$ CFU/year to $3.0x10^{15}$ CFU/year, resulting in an additional nonpoint source load of $1.4x10^{15}$ CFU/year ($\Delta l_{5297665}$) being added to the model at this point. Using Equation F3, we compute an expected increase in mean annual loading from the Aransas River (non-tidal) to the Aransas Tidal River of $2.24x10^{13}$ CFU/yr. Similarly, the expected increase from the Aransas Tidal River to Copano Bay was computed at $2.738x10^{10}$ CFU/year. Table F1 shows the details of the increased loading as it moved through the system, ending with the expected increase to Copano Bay (ΔL_w) of $2.74x10^{10}$ CFU/year.

Results of the TMDL Balance model show that under original conditions ($l_{5297665}$=$1.6x10^{15}$ CFU/year) the load from the Aransas Tidal River to Copano Bay is $5.578345x10^{14}$ CFU/year. Under the new modeled condition (i.e., $l_{5297665}+\Delta l_{5297665}$=$3.0x10^{15}$ CFU/year) this load increases to $5.578618x10^{14}$ CFU/year, equating to a difference in mean annual loading (ΔL_w) of $2.730x10^{10}$ CFU/year. Though the computed increase in loading is not exactly equal to that expected from the calculations shown in Table F1, the discrepancy is considered close enough to be a function of rounding errors. Therefore, based on this analysis, it is confirmed that the TMDL Balance model is working properly.

The second test of the TMDL Balance model was performed on a catchment on the Mission River side of the watershed, catchment 5289427. In this case, the nonpoint

source load travels through one catchment segment, four non-tidal river segments, and five tidal river segments, as shown in Figure F2. The load from catchment 5289427 was increased from 2.43×10^{15} CFU/year to 7.00×10^{15} CFU/year resulting in an expected increase from the Mission Tidal River to Copano Bay of 1.20×10^{9} CFU/year. For this scenario, the modeled increased loading to Copano Bay was 1.20×10^{9} CFU/year, again confirming the proper operation of the model.

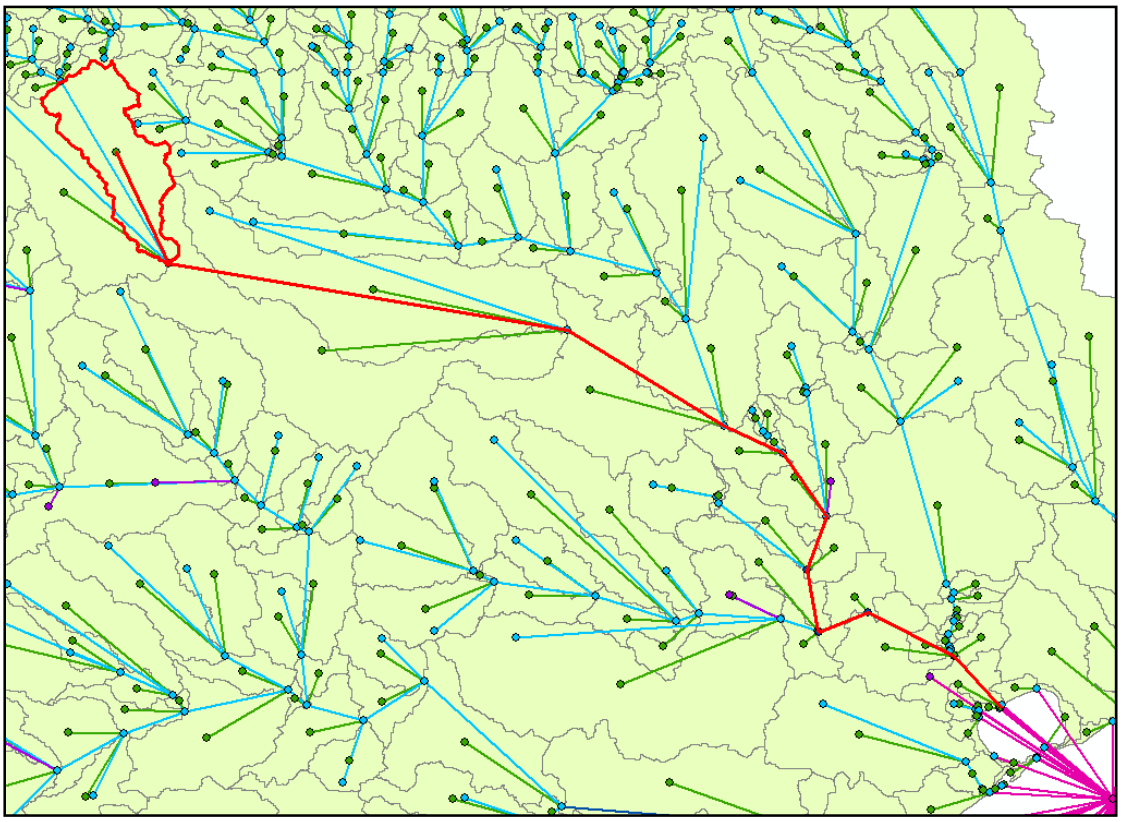


Figure F2: Catchment 5289427 Travel Path to Copano Bay

Model Sensitivity

Given the uncertainty in some of the parameters that were used in modeling the mean annual loading of fecal coliform in the Copano Bay watershed (discussed in Chapters 4 and 5), a sensitivity analysis was performed. This sensitivity analysis is used to quantify the impact that a change in certain modeling parameters would have on the modeled mean fecal coliform concentration in Copano Bay, if all other parameters were kept constant.

The modeled load from failing on-site sewage facilities (OSSFs) that border Copano Bay accounts for a significant percent of the overall bacterial loading to the bay under mean annual conditions. However, as discussed in Chapter 4 and Appendix C a number of assumptions were made to compute the fraction of potential loading from OSSFs that would reach Copano Bay. This fraction is computed as the percent of OSSFs immediately around the bay that fail on a mean annual basis and the percent of potential loading from each of these failing systems that will reach Copano Bay. In this study, we modeled both of these percentages at 50%, so the fraction of potential loading that reaches the bay is modeled at 0.25 (i.e., 0.25 = 0.5*0.5).

Two issues were considered for the analysis of OSSF loadings. First, the impact of changing the fraction of potential loading from OSSFs that entered Copano Bay on the percent of overall loading from the top three sources of fecal coliform to Copano Bay under mean annual conditions was quantified. Table F2 summarizes this analysis, where

the originally modeled fraction is shown in bold. Results show that if the fraction is modeled at 0.025, the loading to Copano Bay from failed OSSFs around the bay reduces to 2% of the overall loading under mean annual conditions. The loadings from deer and beef cattle are adjusted to 24% and 60%, respectively. If the fraction of potential OSSF loading is modeled at 100% (i.e., all systems fail and all of the potential loading enters the bay), failing OSSFs account for 42% of the overall loading to the bay, while deer and beef cattle only account for 14% and 35%, respectively.

Table F2: Impact of Changing OSSF Values on Percent Loading from Three Sources

OSSF Failure Rate (%)	Transmission Rate (%)	Fraction of Potential OSSF Loading	% of Overall Load to Bay from		
			OSSFs	Cattle	Deer
5	50	0.025	1.8	59.8	24.2
50	20	0.1	6.8	56.7	22.9
20	50	0.1	6.8	56.7	22.9
50	50	0.25	15.5	51.5	20.8
70	50	0.35	20.5	48.5	19.6
100	50	0.5	26.9	44.6	18.0
100	100	1	42.3	35.1	14.2

Figure F3 shows the impact of the modeled fractions on the mean concentration of fecal coliform in Copano Bay. The resulting mean concentration varies from 20 to 36 CFU/100ml. An interesting outcome of this analysis is to note that even if the fraction of potential of OSSF loading to Copano Bay was zero (i.e., no systems failed or no load from the failed systems reached the bay), the mean concentration of fecal coliform in

Copano Bay would be approximately 20 CFU/100ml. This is considerably higher than the concentration needed to meet the total maximum daily load (computed in Chapter 5).

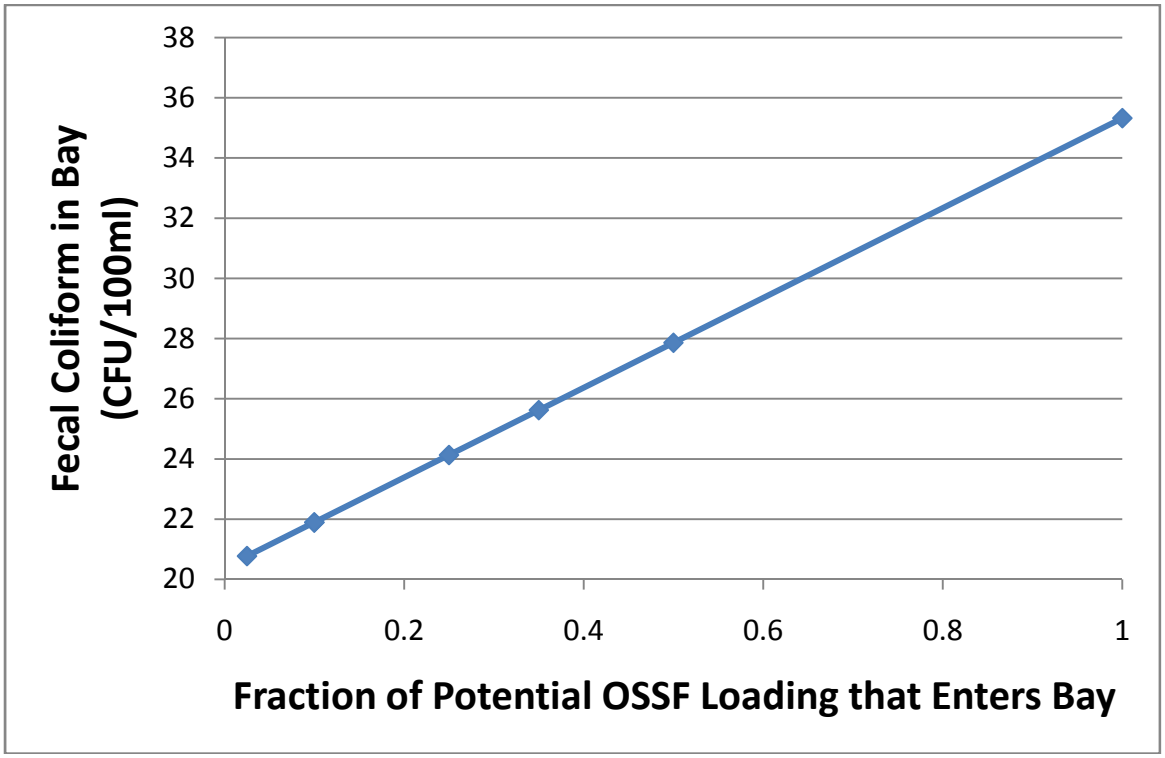


Figure F3: Sensitivity of Model Output to OSSF Assumptions

As discussed in Appendix B, travel times in the tidal river sections of the Mission and Aransas Rivers are computed as a function of tidal river volumes and mean annual flow rates through the segments. Given the number of assumptions that went into computing the tidal river volumes, a sensitivity analysis was performed to quantify the impact of a change in the mean annual tidal river volume (and, therefore, residence time)

on the load of fecal coliform to Copano Bay and the resultant mean concentration in the bay. Figure F4 shows the impact of modeling the tidal river volumes at 25% to 200% of the originally modeled values. The 25% value corresponds to a volume of 1.05×10^6 m^3 in the Aransas Tidal River and a volume of 4.11×10^5 m^3 in the Mission Tidal River. The 100% value is the value that is modeled in the modeling scenario described in Chapters 4 and 5 (i.e., 4.20×10^6 m^3 in the Aransas Tidal River and 1.64×10^6 m^3 in the Mission Tidal River). Results of this analysis show that while fluctuating the tidal river volumes has a notable impact on the fecal coliform loading to Copano Bay; the mean concentration of bacteria in Copano Bay is changed by less than 0.5 CFU/100ml.

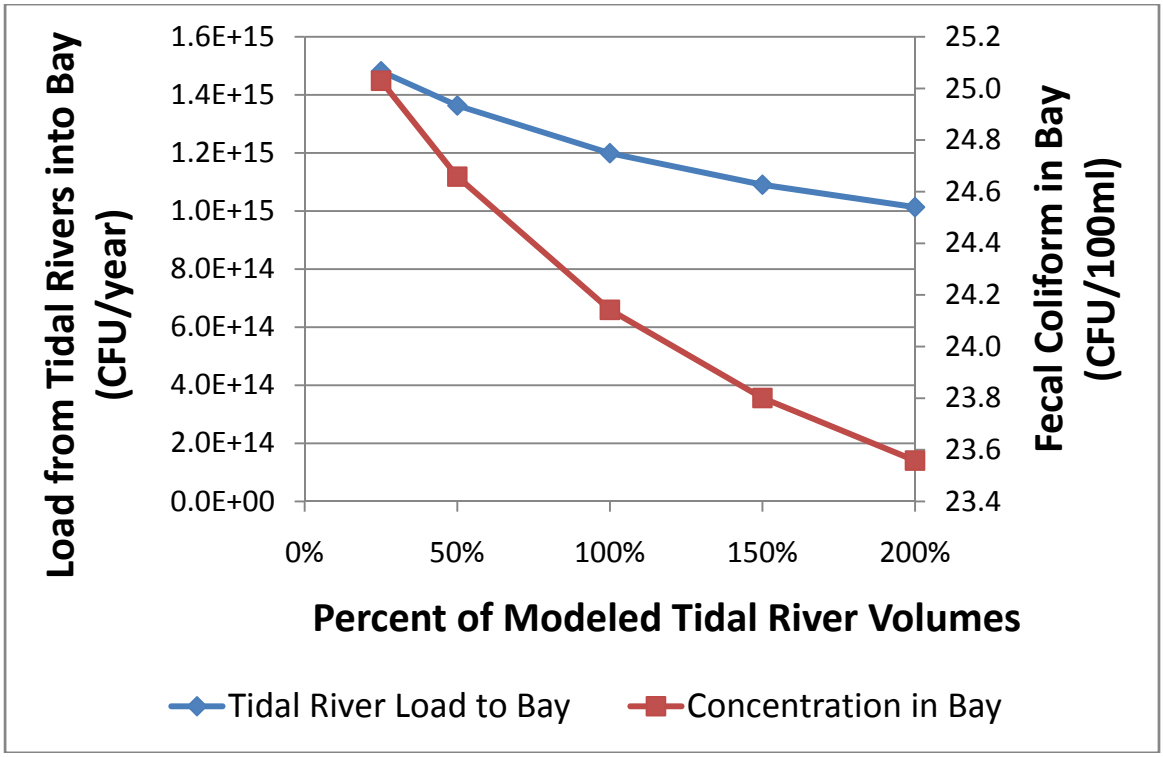
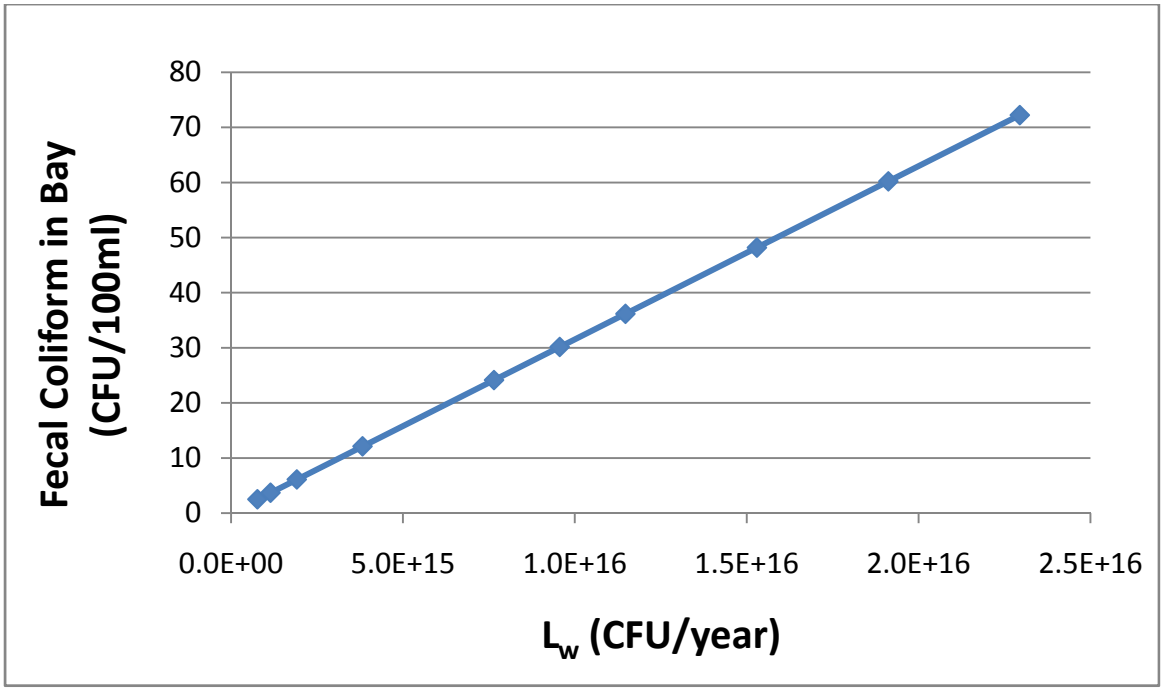
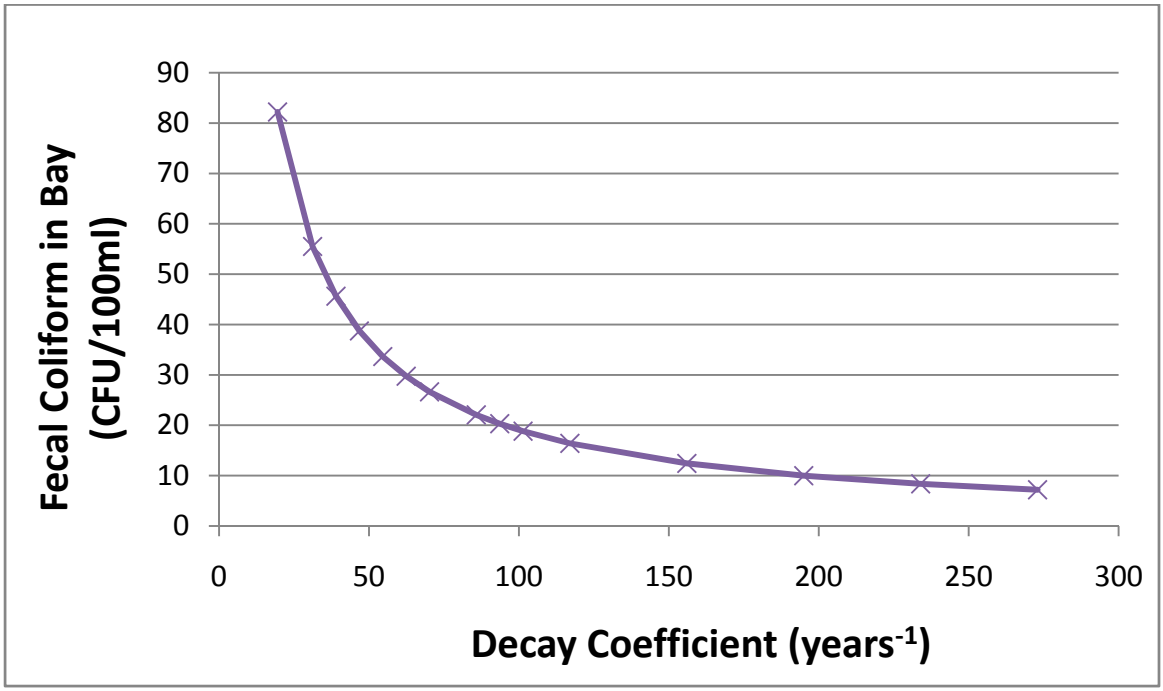
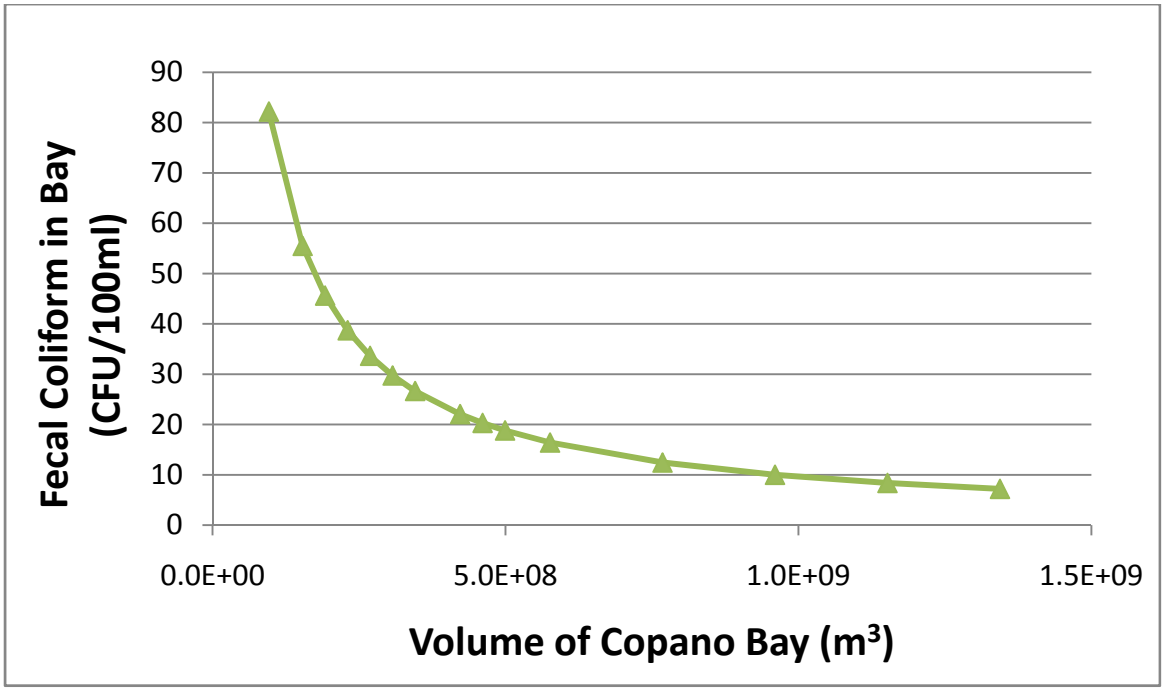


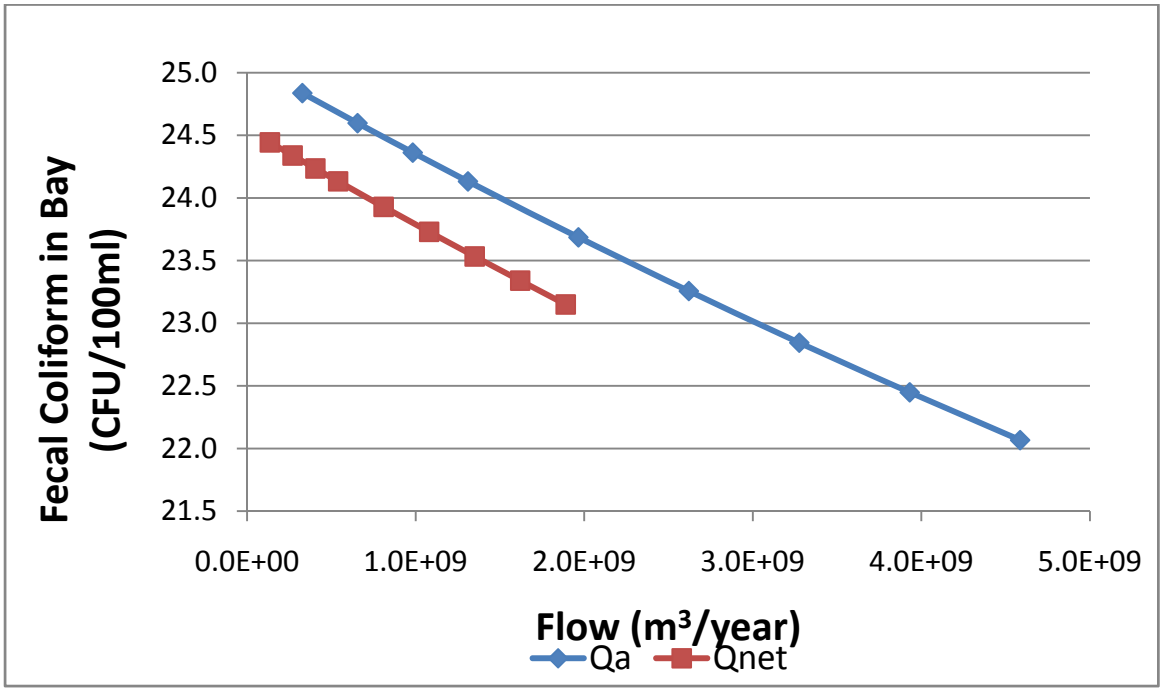
Figure F4: Sensitivity of Model to Tidal River Volumes

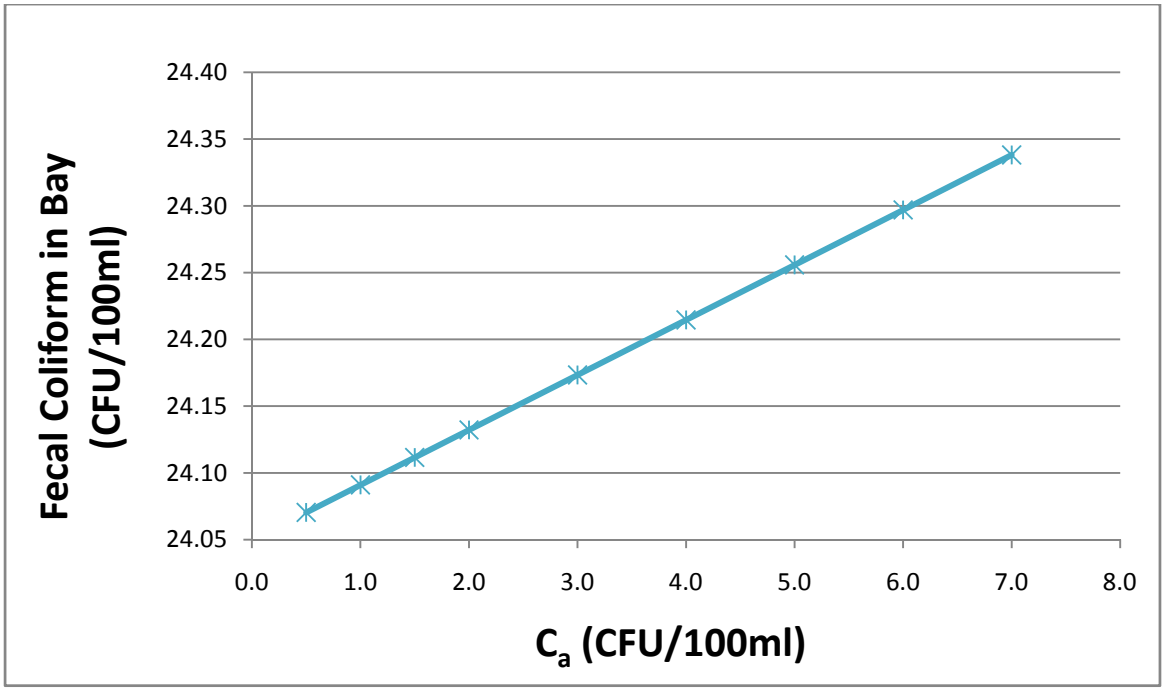
Figures F5 to F9 show the model's sensitivity to the various parameters in the tidal prism equation. Results of this analysis show that the mean concentration of fecal coliform in Copano Bay is most sensitive to the bacterial loading received from the watershed. The concentration is also sensitive to the first-order decay coefficient in the bay and the mean annual volume of the bay. Flows between Copano Bay and Aransas Bay and the concentration of bacteria in Aransas Bay have less of an impact.


Fecal Coliform in Bay (CFU/100ml)
80
70
60
50
40
30
20
10
0
0.0E+00
5.0E+15
1.0E+16
1.5E+16
2.0E+16
2.5E+16
L_w (CFU/year)


Fecal Coliform in Bay (CFU/100ml)
90
80
70
60
50
40
30
20
10
0
0
50
100
150
200
250
300
Decay Coefficient (years^{-1})


Fecal Coliform in Bay (CFU/100ml)
90
80
70
60
50
40
30
20
10
0
0.0E+00
5.0E+08
1.0E+09
1.5E+09
Volume of Copano Bay (m³)


Fecal Coliform in Bay (CFU/100ml)
25.0
24.5
24.0
23.5
23.0
22.5
22.0
21.5
0.0E+00
1.0E+09
2.0E+09
3.0E+09
4.0E+09
5.0E+09
Flow (m³/year)
Qa
Qnet



Figures F5 to F9: Sensitivity of Modeling Results to Tidal Prism Equation Parameters

List of Acronyms and Abbreviations

ACES – Analytical Framework for Coastal and Estuarine Study

BST – bacteria source tracking

CFU – colony forming units

CN – curve number

CRWR – Center for Research in Water Resources

CSTR – continuously stirred tank reactor

CUAHSI – Consortium of Universities for the Advancement of Hydrologic Science, Inc.

DLL – dynamic link library

DSHS – Texas Department of State Health Services

EMC – expected mean concentration

GIS – geographic information systems

KDHE – Kansas Department of Health and Environment

LA – load allocation

LULC – land use/land cover

MOS – margin of safety

MSI – Marine Science Institute

NDEQ – Nebraska Department of Environmental Quality

NHD – National Hydrography Dataset

NLCD – National Land Cover Dataset

NPDES – National Pollutant Discharge Elimination System

NRC – National Research Council

NRCS – Natural Resources Conservation Service

NWIS – National Water Information System

ODEQ – Oklahoma Department of Environmental Quality

ppt – parts per thousand

ROS – regression on order statistics

SWAT – Soil and Water Assessment Tool

SWQM – surface water quality monitoring

SWQMIS – Surface Water Quality Monitoring Information System (formerly TRACS)

TAMUCC – Texas A&M University – Corpus Christi

Task Force – Bacteria TMDL Task Force

TNRCC – Texas Natural Resource Conservation Commission (now the TCEQ)

TCEQ - Texas Commission on Environmental Quality (formerly the TNRCC)

TCOON - Texas Coastal Oceanic Observation Network

TMDL - total maximum daily load

TNRIS - Texas Natural Resources Information System

TRACS – Texas Regulatory Activity and Compliance System (now SWQMIS)

TSSWCB – Texas State Soil and Water Conservation Board

USEPA – U.S. Environmental Protection Agency

USGS – U.S. Geological Survey

UT – University of Texas

VB – Visual Basic

VBA – Visual Basic for Applications

WLA – waste load allocation

WWTP – wastewater treatment plant

Works Cited

Bacteria TMDL Task Force, 2007. Bacteria Total Maximum Daily Load Task Force Report. Texas Commission on Environmental Quality and Texas State Soil and Water Conservation Board, College Station, TX, 101p.

Blackland Research and Extension Center, and T. A. M. U. System, 2007. Soil and Water Assessment Tool: SWAT. http://www.brc.tamus.edu/swat/index.html. Accessed: July 2007.

Brissaud, F., V. Lazarova, C. Ducoup, C. Joseph, B. Levine, and M. G. Tournoud, 2000. Hydrodynamic Behaviour and Faecal Coliform Removal in a Maturation Pond. *Water Science and Technology*, 42(10-11):119-126.

Chapra, S. C., 2003. Engineering Water Quality Models and TMDLs. *Journal of Water Resources Planning and Management*, 129(4):247-256.

Chow, V. T., D. R. Maidment, and L. W. Mays, 1988. *Applied Hydrology*, McGraw-Hill, New York.

Christensen, V. G., P. P. Rasmussen, A. C. Ziegler, and X. Jian, 2001. Continuous Monitoring and Regression Analysis to Estimate Bacteria Loads. In: *Proceedings of TMDL Science Issues Conference*, Water Environment Federation, St. Louis, Missouri, 405-411.

Cleland, B., 2002. TMDL Development from the "Bottom Up" – Part II: Using Duration Curves to Connect the Pieces. In: *National TMDL Science and Policy 2002 – WEF Specialty Conference*, Water Environment Federation, Phoenix, AZ.

Cleland, B., 2003. TMDL Development from the "Bottom Up" – PART III: Durations Curves and Wet-Weather Assessments In: *National TMDL Science and Policy 2003 - WEF Specialty Conference*, Chicago, IL, 27.

Cogger, C., L. Hajjar, C. Moe, and M. Sobsey, 1988. Septic System Performance on a Coastal Barrier Island. *Journal of Environmental Quality*, 17(3):401-408.

Consortium of Universities for the Advancement of Hydrologic Sciences, 2007. WaterOneFlow Services. http://water.sdsc.edu/wateroneflow/. Accessed: December, 2007.

Dyer, K. R., 1973. *Estuaries: A Physical Introduction*, John Wiley & Sons, London.

Engelking, G., 2009. Refugio County Groundwater Conservation District.

Erkenbrecher, C. W., Jr., 1981. Sediment bacterial indicators in an urban shellfishing subestuary of the lower Chesapeake Bay. *Applied and Environmental Microbiology*, 42(3):484-492.

ESRI, 2007. Arc Hydro Tools v1.2 - Tutorial. ESRI, Redlands, CA, 114p.

Fischer, H. H., E. J. List, R. C. Y. Koh, J. Imberger, and N. H. Brooks, 1979. *Mixing in Inland and Coastal Waters*, Academic Press, Inc., New York.

Gannon, J. J., and M. K. Busse, 1989. E. coli and Enterococci Levels in Urban Stormwater, River Water and Chlorinated Treatment Plant Effluent. *Water Research*, 23(9):1167-1176.

Gibson, C. J. (2006). "Bacterial Loadings Watershed Model in Copano Bay," M.S. Thesis. The University of Texas at Austin, Austin.

Goyal, S. M., C. P. Gerba, and J. L. Melnick, 1977. Occurrence and distribution of bacterial indicators and pathogens in canal communities along the Texas coast. *Applied and Environmental Microbiology*, 34(2):139-149.

Hagedorn, C., E. McCoy, and T. Rahe, 1981. The Potential for Ground Water Contamination from Septic Effluents. *Journal of Environmental Quality*, 10(1):1-8.

Hampson, J., and S. Bourne, 2007. ACES - Analytical Framework for Coastal and Estuarine Study, Part I: Conceptual Approach. Post, Buckley, Schuh and Jernigan (PBS&J), Tampa, FL.

Helsel, D. R., 2005. *Nondetects and Data Analysis: Statistics for Censored Evironmental Data*, John Wiley & Sons, Inc., Hoboken, New Jersey.

Horizon Systems, 2007. National Hydrography Dataset Plus. http://www.horizon-systems.com/nhdplus/. Accessed: August, 2007.

Hydroscience Inc., 1978. An Assessment of Non-point Sources of Pollution in the Southeast Texas Designated Planning Area.

Hyland, R., J. Byrne, B. Selinger, T. Graham, J. Thomas, I. Townshend, and V. Gannon, 2003. Spatial and Temporal Distribution of Fecal Indicator Bacteria within the Oldman River Basin of Southern Alberta, Canada. *Water Quality Research Journal of Canada*, 38(1):15-32.

Jamieson, R. C., R. J. Gordon, S. C. Tattrie, and G. W. Stratton, 2003. Sources and Persistence of Fecal Coliform in a Rural Watershed. *Water Quality Research Journal of Canada*, 38(1):33-47.

Jobson, H. E., 1996. Prediction of Traveltime and Longitudinal Dispersion in Rivers and Streams. *U.S. Geological Survey Water Resources Investigations Report 96-4013*, U.S. Geological Survey, 72p.

Johnson, S., T. Whiteaker, and D. Maidment, 2009. A Tool for Automated Load Duration Curve Creation. *Journal of the American Water Resources Association,* 45(3): 654-663.

Kansas Department of Health and Environment, 2008. Total Maximum Daily Loads (TMDLs). http://www.kdheks.gov/tmdl/index.htm. Accessed: July, 2008.

Kaplan, B. O., 1987. *Septic Systems Handbook*, Lewis Publishers, Inc., Chelsea, Michigan.

Kapur, K. C., and L. R. Lamberson, 1977. *Reliability in Engineering Design*, John Wiley & Sons, Inc., New York.

Ketchum, B. H., 1951. The Exchanges of Fresh and Salt Waters in Tidal Estuaries. *Journal of Marine Research*, 10(1):18-38.

Kloot, R. W., B. Radakovich, X. Huang, and D. D. Brantley, 2006. A Comparison of Bacterial Indicators and Methods in Rural Surface Waters. *Environmental Monitoring and Assessment*, 121:275-287.

Kuo, A. Y., and B. J. Neilson, 1988. A Modified Tidal Prism Model for Water Quality in Small Coastal Embayments. *Water Science & Technology*, 20(6/7):133-142.

Kuo, A. Y., K. Park, S.-C. Kim, and J. Lin, 2005. A Tidal Prism Water Quality Model for Small Coastal Basins. *Coastal Management*, 33(1):101 - 117.

Lawson, L. G., 2003. Guidance Memo No. 03-2012; HSPF Model Calibration and Verification for Bacteria TMDLs. Commonwealth of VA Department of Environmental Quality, ed., 28.

Maidment, D., 2002. *ArcHydro: GIS for Water Resources*, ESRI Press, Redlands, CA.

Maidment, D., 2008. CUAHSI Hydrologic Information System: Overview of Version 1.1 CUAHSI, Austin, TX, 92p.

Maidment, D. R., 1992. *Handbook of Hydrology*, McGraw-Hill, Inc., New York.

Matson, E. A., S. G. Hornor, and J. D. Buck, 1978. Pollution indicators and other microorganisms in river sediment. *Journal - Water Pollution Control Federation* 50(1):13-19.

Mays, L. W., 2001. *Water Resources Engineering*, 1 Ed., John Wiley & Sons, Inc., Hoboken, NJ.

McBride, G. B., 2005. *Using Statistical Methods for Water Quality Management: Issues, Problems, and Solutions*, John Wiley & Sons, Inc, Hoboken, New Jersey.

McClelland, J., 2008. Personal Communication. Port Aransas, TX.

Moench, E., and K. Wagner, 2009. Education Program for Improved Water Quality in Copano Bay: Task Two Report. Texas Water Resources Institute, 26p.

Mooney, R., 2008. Nitrogen dynamics during and after storm events in the Mission-Aransas NERR. The University of Texas Marine Science Institute, Port Aransas, TX.

Mott, J. B., and R. L. Lehman, 2005. Bacteria Source Tracking in Copano Bay: Phase II - Final Report Texas A&M University - Corpus Christi, 190p.

National Research Council, 2001. Assessing the TMDL Approach to Water Quality Management. National Academy of Sciences, Washington, D.C., 103p.

Nebraska Department of Environmental Quality, 2008. Impaired Waters and Total Maximum Daily Loads (TMDLs). http://www.deq.state.ne.us/SurfaceW.nsf/Pages/TMDL. Accessed: July, 2008.

Noble, R. T., D. F. Moore, M. K. Leecaster, C. D. McGee, and S. B. Weisberg, 2003. Comparison of Total Coliform, Fecal Coliform, and Enterococcus Bacterial Indicator Response for Ocean Recreational Water Quality Testing. *Water Research*, 37:1637-1643.

Nueces River Authority, 2008. Surface Water Quality Monitoring to Support the Copano Bay Total Maximum Daily Load for Bacteria in Oyster Waters: Quality Assurance Project Plan. Revision #1. Corpus Christi, TX.

Oklahoma Department of Environmental Quality, 2008. TMDLs & Water Quality Modeling. http://www.deq.state.ok.us/wqdnew/tmdl/index.html. Accessed: July, 2008.

Oregon State University PRISM Group, 2008. PRISM (Parameter-elevation Regressions on Independent Slopes Model) Group. http://www.prism.oregonstate.edu/. Accessed: March, 2009.

Petersen, T., C. W. Sowells, H. S. Rifai, and R. Stein, 2008. Comparisons of Methods to Calculate TMDLs for E. coli: Load Duration Curves, Mass Balance, and HSPF. In: *World Environmental and Water Resources Congress 2008 Ahupua'a*, American Society of Civil Engineers, Honolulu, HI.

Petersen, T. M., H. S. Rafai, M. P. Suarez, and A. R. Stein, 2005. Bacteria Loads from Point and Nonpoint Sources in an Urban Watershed. *Journal of Environmental Engineering*, 131(10):1414-1425.

Quenzer, A. M., and D. R. Maidment. (1998). "A GIS Assessment of the Total Loads and Water Quality in the Corpus Christi Bay System," University of Texas, Austin.

Reneau, R., and D. Pettry, 1975. Movement of Coliform Bacteria from Septic Tank Effluent through Selected Coastal Plan Soils of Virginia. *Journal of Environmental Quality*, 4(1):41-44.

Shabman, L., K. Reckhow, M. B. Beck, J. Benaman, S. Chapra, P. Freedman, M. Nellor, J. Rudek, D. Schwer, T. Stiles, and C. Stow, 2007. Adaptive Implementation of Water Quality Improvement Plans: Opportunities and Challenges. Nicholas School of the Environment and Earth Sciences, 99p.

Shen, J., S. Sun, and T. Wang, 2005. Development of the Fecal Coliform Total Maximum Daily Load Using Loading Simulation Program C ++ and Tidal Prism Model in Estuarine Shellfish Growing Areas: A Case Study in the Nassawadox Coastal Embayment, Virginia. *Journal of Environmental Science & Health, Part A: Toxic/Hazardous Substances & Environmental Engineering*, 40(9):1791-1807.

Shiaris, M. P., A. C. Rex, G. W. Pettibone, K. Keay, P. McManus, M. A. Rex, J. Ebersole, and E. Gallagher, 1987. Distribution of indicator bacteria and Vibrio parahaemolyticus in sewage-polluted intertidal sediments. *Applied and Environmental Microbiology* 53(8):1756-1761.

Soil Survey Staff, N. R. C. S., United States Department of Agriculture, 2008a. Soil Survey Geographic (SSURGO) Database for Texas. http://soildatamart.nrcs.usda.gov. Accessed: January 14, 2009.

Soil Survey Staff, N. R. C. S., United States Department of Agriculture, 2008b. Web Soil Survey. http://websoilsurvey.nrcs.usda.gov/. Accessed: January 15, 2009.

Stewart, L., and R. Reneau, 1981. Spatial and Temporal Variation of Fecal Coliform Movement Surrounding Septic Tank-Soil Absorption Systems in Two Atlantic Coastal Plain Soils. *Journal of Environmental Quality*, 10(4):528-531.

Sullivan, A., and F. Hambleton, 2007. Application of Load Allocation Tools for the Development of Total Maximum Daily Loads (TMDLs) for Bacteria in Texas: Comparison Between Empirical and Dynamic Modeling Approaches. In: *Water Environment Federation TMDL 2007*, Water Environment Federation, Seattle, WA.

Texas A&M University - Corpus Christi, 2007. Texas Coastal Ocean Observation Network. http://lighthouse.tamucc.edu/TCOON/HomePage. Accessed: July, 2007.

Texas Commission on Environmental Quality, 2007a. 2006 Texas 303(d) List Texas Commission on Environmental Quality, Austin, TX, 119p.

Texas Commission on Environmental Quality, 2007b. On-Site Activity Reporting System (OARS). http://www.tceq.state.tx.us/compliance/compliance_support/regulatory/ossf/on-site-activity-reporting-system/OARS.html. Accessed: June, 2008.

Texas Commission on Environmental Quality, 2007c. Sampling Data Query, Surface Water Quality Monitoring. http://www.tceq.state.tx.us/compliance/monitoring/crp/data/samplequery.html. Accessed: July, 2007.

Texas Commission on Environmental Quality, 2008. 2008 Guidance for Assessing and Reporting Surface Water Quality in Texas. Texas Commission on Environmental Quality, Austin, 170p.

Texas Department of State Health Services Seafood and Aquatic Life Group, 2006. Comprehensive Sanitary Survey of the Shellfish Producing Waters of Copano Bay 21p.

Texas Department of State Health Services Seafood and Aquatic Life Group, 2007. Annual Update of the Shellfish Producing Waters of Aransas and Copano Bays 13p.

Texas Natural Resource Conservation Commission, 2000. Chapter 307: Texas Surface Water Quality Standards. 142.

Texas Natural Resources Information System, 2008. TNRIS Completes the Acquisition of High-Resolution Data for Areas on the Texas Coast. http://www.tnris.state.tx.us/news.aspx?id=724. Accessed: January 18, 2008.

Texas Water Development Board, 2008. Evaporation/Precipitation Data for Texas. http://midgewater.twdb.state.tx.us/Evaporation/evap.html. Accessed: June, 2008.

Traister, E., and S. C. Anisfeld, 2006. Variability of Indicator Bacteria at Different Time Scales in the Upper Hoosic River Watershed. *Environmental Science and Technology*, 40(16):4990-4995.

Tufford, D. L., and W. D. Marshall, 2002. Fecal Coliform Source Assessment in a Small, Mixed Land Use Watershed. *Journal of the American Water Resources Association*, 38(6):1625-1635.

U.S. Army Corps of Engineers Hydrologic Engineering Center, 2003. Geospatial Hydrologic Modeling Extension: HEC-GeoHMS. 281p.

U.S. Army Corps of Engineers Hydrologic Engineering Center, 2005. HEC-GeoRAS: GIS Tools for Supoort of HEC-RAS using ArcGIS. 204p.

U.S. Department of Agriculture Natural Resources Conservation Service, 1986. Urban Hydrology for Small Watersheds, Technical Release TR-55.

U.S. Environmental Protection Agency, 1986. Ambient Water Quality Criteria for Bacteria EPA440/5-84-002. 18p.

U.S. Environmental Protection Agency, 2001. Protocol for Developing Pathogen TMDLs. Office of Water (4503F), U.S. Environmental Protection Agency, Washington, D.C., 132p.

U.S. Environmental Protection Agency, 2002. Onsite Wastewater Treatment Systems Manual. 367p.

U.S. Environmental Protection Agency, 2007. An Approach for Using Load Duration Curves in Developing TMDLs. U.S. Environmental Protection Agency: Office of Wetlands, Oceans, & Watersheds, Washington, DC, 68p.

U.S. Environmental Protection Agency, 2008a. Envirofacts - Water Discharge Permits (PCS). http://www.epa.gov/enviro/html/pcs/pcs_query_java.html. Accessed: April 18, 2008.

U.S. Environmental Protection Agency, 2008b. US Environmental Protection Agency Total Maximum Daily Loads. http://www.epa.gov/owow/tmdl/. Accessed: February, 2008.

U.S. Geological Survey, 2007a. National Hydrography Dataset. http://nhd.usgs.gov/. Accessed: August, 2007.

U.S. Geological Survey, 2007b. National Land Cover Dataset 1992 (NLCD 1992). http://landcover.usgs.gov/natllandcover.php. Accessed: 2008.

U.S. Geological Survey, 2007c. NWIS Daily Values Web Service -- Beta 1.0. http://waterdata.usgs.gov/nwis/?DailyValues_Service_Instructions. Accessed: January, 2008.

U.S. Geological Survey, 2007d. US Geological Survey National Water Information System. http://waterdata.usgs.gov/nwis. Accessed: July, 2007.

U.S. Geological Survey, 2008. National Land Cover Database 2001 (NLCD 2001). http://www.mrlc.gov/nlcd.php. Accessed: December, 2008.

US Fish and Wildlife Service, 2003. Texas Colonial Waterbird Census. http://www.fws.gov/texascoastalprogram/TCWC.htm. Accessed: June, 2008.

Valiela, I., M. Alber, and M. Lamontagne, 1991. Fecal Coliform Loadings and Stocks in Buttermilk Bay, Massachusetts, USA, and Management Implications. *Environmental Management* 15(5):659-674.

Virginia Department of Environmental Quality, 2005. Urbanna Creek Total Maximum Daily Load (TMDL) Report for Shellfish Condemnation Areas Listed Due to Bacteria Contamination: Draft. Virginia Department of Environmental Quality, 74p.

Vogel, R. M., and N. M. Fennessey, 1995. Flow Duration Curves II: A Review of Applications in Water Resources Planning. *Water Resources Bulletin*, 31(6):1029-1039.

Ward, G., 1997. Processes and Trends of Circulation within the Corpus Christi Bay National Estuary Program Study Area.

Whiteaker, T., 2008. HydroObjects Version 1.1. CUAHSI, Austin, TX, 11p.

Whiteaker, T. L., D. R. Maidment, J. L. Goodall, and M. Takamatsu, 2006. Integrating Arc Hydro Features with a Schematic Network. *Transactions in GIS*, 10(2):219-237.

World Wide Web Consortium, 2004. Web Services Architecture. http://www.w3.org/TR/ws-arch/. Accessed: July, 2008.

Zoun, R. J. (2003). "Estimation of Fecal Coliform Loadings to Galveston Bay," Master's Thesis, The University of Texas at Austin, Austin, TX.

Vita

Stephanie L. Johnson was born on June 7, 1977 in Minneapolis, Minnesota to Steven and Lynn Johnson. She has one older brother, Charlie, and one younger sister, Ashley. Stephanie enrolled at the University of Wisconsin – Platteville in the fall of 1995 and earned a double major in Civil and Environmental Engineering with a minor in Philosophy in 2000. Over the next four years she traveled, worked as an environmental engineer in the Western United States, and earned a Masters Degree in Civil Engineering from the University of Minnesota in 2004. Stephanie spent two more years working as an engineering consultant in Las Cruces, New Mexico before returning to graduate school to pursue a doctoral degree at the University of Texas at Austin in 2006. Stephanie married Angela Ronay on December 22, 2006. Stephanie has published two articles in peer-reviewed journals: one addressing the change in Minnesota's water resources as a consequence of climate variation and the other on the LDCurve tool which automates the creation of load duration curves. Stephanie looks forward to returning to the Midwestern United States upon completing her degree.

Permanent address: 4179 Maureen Drive, Minneapolis, Minnesota 55421

This dissertation was typed by the author.